

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:50 ; Search time 53.9852 Seconds
(without alignments)
1584.263 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLAAMWTARALEV.....KMQQNGYENPTYKFFEQMGN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 segs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4058	100.0	770	10	Novel amyloid prec
2	4058	100.0	770	14	Mutated APP770 exo
3	4058	100.0	770	15	AAAR63442
4	4058	100.0	770	19	AAAW40130
5	4058	100.0	770	20	AAAW97996
6	4058	100.0	770	22	AAAE10648
7	4058	100.0	770	22	AAAE11762
8	4058	100.0	770	22	AAAE06893
9	4058	100.0	770	22	AAAU06622
10	4058	100.0	770	22	AAAE02600
11	4058	100.0	772	22	AAAE10650

12	4058	100.0	772	22	AAE06895	Human amyloid prec
13	4058	100.0	772	22	AAU06624	Human Amyloid prec
14	4058	100.0	772	22	AAU07223	Human beta-amyloid
15	4058	100.0	772	22	AAE02602	Human amyloid prec
16	4054	99.9	770	15	AAAR62505	Amyloid precursor
17	4053	99.9	770	18	AAW19500	APP770 mutant A-be
18	4053	99.9	770	18	AAW19497	APP770 mutant A-be
19	4053	99.9	770	18	AAW19485	APP770 mutant A-be
20	4053	99.9	770	18	AAW19482	APP770 mutant A-be
21	4053	99.9	770	22	AAE06912	Human amyloid prec
22	4050	99.8	770	22	AAE06912	Human amyloid prec
23	4047	99.7	770	18	AAW19506	APP770 mutant A-be
24	4047	99.7	770	18	AAW19491	APP770 mutant A-be
25	4046	99.7	770	13	AAAR26340	APP770. Homo sapi
26	4046	99.7	770	18	AAW19488	APP770 mutant A-be
27	4046	99.7	770	18	AAW19503	APP770 mutant A-be
28	4039	99.5	770	11	AAAR05717	APP770 mutant A-be
29	3943.5	97.2	751	12	AAAR10022	NAP gene product a
30	3943.5	97.2	751	13	AAAR20328	Beta-amyloid-relat
31	3943.5	97.2	751	20	AAAY08615	Human beta-amyloid
32	3943.5	97.2	751	20	AAAY08605	Human beta-amyloid
33	3943.5	97.2	751	22	AAAE10649	Human amyloid prec
34	3943.5	97.2	751	22	AAAE06894	Human amyloid prec
35	3943.5	97.2	751	22	AAU06623	Human partial Amyl
36	3943.5	97.2	751	22	AAE02601	Human amyloid prec
37	3943.5	97.2	753	22	AAAE10651	Human amyloid prot
38	3943.5	97.2	753	22	AAE06896	Human amyloid prec
39	3943.5	97.2	753	22	AAU06625	Human Amyloid prec
40	3943.5	97.2	753	22	AAU07224	Human beta-amyloid
41	3943.5	97.2	753	22	AAE02603	Human amyloid prec
42	3938.5	97.1	751	18	AAW19486	APP751 mutant A-be
43	3938.5	97.1	751	18	AAW19496	APP751 mutant A-be
44	3938.5	97.1	751	18	AAW19499	APP751 mutant A-be
45	3938.5	97.1	751	18	AAW19483	APP751 mutant A-be

ALIGNMENTS

RESULT 1					
AAP94775					
ID	AAP94775 standard; protein; 770 AA.				
XX					
AC	AAP94775;				
XX					
DT	05-JUL-1990 (first entry)				
XX					
DE	Novel amyloid precursor protein (NAP).				
XX					
KW	SPAP; amyloid precursor protein; dysbolism; INS76; ds.				
XX					
OS	Homo sapiens.				
XX					
FH	Key				Location/Qualifiers
FT	Active-site				289..345
FT					/*tag= a
FT					/*label=INS76
XX					
PN	EP304013-A.				
XX					
PD	22-FEB-1989.				
XX					
PF	16-AUG-1988;				88EP-0113283.
XX					
PR	15-AUG-1987;				87JP-0203298.
PR	21-AUG-1987;				87JP-0207995.
PR	18-NOV-1987;				87JP-0291404.
PR	11-DEC-1987;				87JP-0313228.
PR	05-FEB-1988;				88JP-0025260.
PR	10-FEB-1988;				88JP-0029366.
PR	19-FEB-1988;				88JP-0037905.
PR	25-MAY-1988;				88JP-0125660.
XX					

PA (ASAH) ASAH KASEI KOGYO.
XX
PI Kitaguchi N, Takahashi Y, Tokushima Y, Itoh H;
XX
DR WPI: 1989-055458/08.
DR N-PSDB; AAN91049.
XX
PT Human senile plaque amyloid precursor protein and DNA -
PT used for study and diagnosis of dysbolism in the central nervous
PT system.
XX
XX Disclosure; ; 108bp; English.
PS
CC AA. sequence from 289 to 345 encodes INS76 which is claimed as a senile
CC plaque amyloid precursor (SPAP), useful for diagnosis of dysbolism in the
CC CNS such as senile dementia.
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 10; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGALLLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYQOEYVPELQITNVVEANQPTIQNMCKRGKCKTHPHFVPIPYRCLVG 120
DB 61 TCIDTKEGILQYQOEYVPELQITNVVEANQPTIQNMCKRGKCKTHPHFVPIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDVSDADEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESDNDVSDADEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDEGEVEEAEPEYEATERETSTATTTTTSVEEVEVREYVCEQAETGPC 300
DB 241 EADDEDEDEGEVEEAEPEYEATERETSTATTTTTSVEEVEVREYVCEQAETGPC 300
QY 301 RAMISRWFYDVTGKCAFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPPLARD 360
DB 301 RAMISRWFYDVTGKCAFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPPLARD 360
QY 361 PVKLPTTAASPDVAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREWEAEARQA 420
DB 361 PVKLPTTAASPDVAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREWEAEARQA 420
QY 421 KNLPKADKKAVALQHFQEKVESLEQEAANERQOLVETMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPKADKKAVALQHFQEKVESLEQEAANERQOLVETMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVYTHLRVIYER 540
DB 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVYTHLRVIYER 540
QY 541 MNQSLSLYNPAVAEEIQDEVEDELLQKEQNSDDVLANMISEPRISYGDALMPSLTET 600
DB 541 MNQSLSLYNPAVAEEIQDEVEDELLQKEQNSDDVLANMISEPRISYGDALMPSLTET 600
QY 601 KTTVELLPVNGEESLDDLPWHSFGADSVPAANTENEVEVPDARPAADRGILTTRPGSGLTN 660
DB 601 KTTVELLPVNGEESLDDLPWHSFGADSVPAANTENEVEVPDARPAADRGILTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLWGVVIAIVITL 720
DB 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLWGVVIAIVITL 720
QY 721 VMLKKQYTSIHGVVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMN 770
DB 721 VMLKKQYTSIHGVVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMN 770

DB 721 VMLKKQYTSIHGVVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMN 770
RESULT 2
AAR41546
ID AAR41546 standard; Protein; 770 AA.
XX
XX AAR41546;
AC
XX 15-MAR-1994 (first entry)
DT
XX
DE Mutated APP770 exon 17 protein fragment.
XX
KM Probe; mutation; exon 17; amyloid precursor protein; APP770;
KM substitution; progressive presenile dementia; Alzheimer's disease;
KM cerebral haemorrhage; cerebral amyloid angiopathy; 4 kD fragment;
KM blood vessels; brain parenchyma; assay; processing; plaque.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Misc-difference 692
FT /note= "position of mutation which causes abnormal processing of APP770"

PD 22-SEP-1993.
XX
XX 20-MAR-1992; 92EP-0400771.
PF 20-MAR-1992; 92EP-0400771.
PR 20-MAR-1992; 92EP-0400771.
PA (INNO-) INNOGENETICS NV SA.
XX
PI Cras P, Hendriks L, Martin J, Van Broeckhoven C;
XX
DR WPI: 1993-296442/38.
DR N-PSDB; AAQ48860.
XX
PT New mutant form of beta-amyloid polypeptide - related to
PT development of cerebral haemorrhage and Alzheimer's disease, also
PT corresp. nucleic acid, vectors, host cells and antibodies
XX
PS Disclosure; Fig 4; 21pp; English.
XX
CC This sequence is encoded by exon 17 of the amyloid precursor protein
CC APP770. A mutation at position 2075 of the DNA sequence, a C>G
CC substitution, causes the substitution of Ala for Gly at codon 692.
CC This mutation has been detected in related patients with progressive
CC presenile dementia (Alzheimer's disease) or cerebral haemorrhage due
CC to cerebral amyloid angiopathy. It may be responsible for the
CC deposition of a 4 kD proteolytic fragment of APP in blood vessel
CC walls and brain parenchyma. Probes specific for the mutation (see
CC also AAQ48858-59) can be used to assay mRNA encoding substances which
CC cause abnormal processing of APP related to plaque formation, and to
CC detect this specific mutation.
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 14; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGALLLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYQOEYVPELQITNVVEANQPTIQNMCKRGKCKTHPHFVPIPYRCLVG 120
DB 61 TCIDTKEGILQYQOEYVPELQITNVVEANQPTIQNMCKRGKCKTHPHFVPIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

|||||
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTTSIAITTTTSTESVEEVREVCSQAETGPC 300
241 EADDEDEDGDEVEEEAEPEYEATERTTSIAITTTTSTESVEEVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTTSIAITTTTSTESVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYCGSAMSQSLKTQEPPLARD 360
301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYCGSAMSQSLKTQEPPLARD 360
Db 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYCGSAMSQSLKTQEPPLARD 360
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
Db 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
Db 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVPAVAEEIQDEVDLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
541 MNQSLSLYNPVPAVAEEIQDEVDLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVPAVAEEIQDEVDLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFSLDLQPMHSGADSVPAANTENEVEPVDPADRGLTTRPGSGLTN 660
601 KTTVELLPVNGEFSLDLQPMHSGADSVPAANTENEVEPVDPADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDLQPMHSGADSVPAANTENEVEPVDPADRGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVNHQKLVFAEDVGSNKGAIIGLMVGVVIAIVITL 720
661 IKTEEISEVKMDAEFRHDSGYEVNHQKLVFAEDVGSNKGAIIGLMVGVVIAIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVNHQKLVFAEDVGSNKGAIIGLMVGVVIAIVITL 720
QY 721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 770
721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 770
Db 721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 770
RESULT 3
AAR63442
D AAR63442 standard; protein; 770 AA.
C AAR63442;
XX 30-JUN-1995 (first entry)
DT Amyloid protein precursor App.
XX Amyloid protein precursor App.
DE Amyloid protein precursor App.
XX Amyloid protein precursor; APP; beta-amyloid protein; gelatinase A;
KW progelatinase A; decomposing agent; prophylaxis; Alzheimer's disease.
XX Homo sapiens.
OS
XX
FH Key
FT Region
FT Location/Qualifiers
FT 672..711
FT /note= "beta-Ap 1-40 gelatinase A
FT cleavage sites"
FT Cleavage-site 687..689
FT /label= gelatinase A
FT Cleavage-site 701..702
FT /label= gelatinase A
FT Cleavage-site 705..706
FT /label= gelatinase A
XX
PN EP622079-A.
XX
PD 02-NOV-1994.

XX
PF 25-APR-1994; 94EP-0302924.
XX
PR 27-APR-1993; 93JP-0122207.
PR 25-FEB-1994; 94JP-0051133.
XX
PA (ORIV) ORIENTAL YEAST CO LTD.
XX
PI Miyazaki K;
XX
DR WPI; 1994-334379/42.
XX
PT Gelatinase A-contg. amyloid beta protein decomposing agent -
PT useful for prophylaxis or treatment of Alzheimer's disease
XX
PS Disclosure; Fig 1; 12pp; English.
XX
CC AAR63442 describes the amino acid sequence of the amyloid protein
CC precursor (APP), from which beta amyloid protein is derived (APB).
CC An APB decomposing agent having either gelatinase A, a limited
CC decomposite of gelatinase A, or progelatinase A as an active
CC ingredient was developed. This agent can be used in medicine for
CC prophylaxis and for the treatment of Alzheimer's disease.
XX
SQ Sequence 770 AA;
Query Match 100.0%; Score 4058; DB 15; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGIALLLAATARALEVPTDGNAGLLAEPOIAMFCGRMLMNMNVQNGKWDSPSGTK 60
Db 1 MLPGIALLLAATARALEVPTDGNAGLLAEPOIAMFCGRMLMNMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYQCEVYPELIQTNVVEANOPVTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120
Db 61 TCIDTKEGILQYQCEVYPELIQTNVVEANOPVTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTTSIAITTTTSTESVEEVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTTSIAITTTTSTESVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYCGSAMSQSLKTQEPPLARD 360
Db 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYCGSAMSQSLKTQEPPLARD 360
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
Db 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
Db 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVPAVAEEIQDEVDLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVPAVAEEIQDEVDLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFSLDLQPMHSGADSVPAANTENEVEPVDPADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDLQPMHSGADSVPAANTENEVEPVDPADRGLTTRPGSGLTN 660

OY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIIGLMGVVIATYIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIIGLMGVVIATYIVITL 720
OY 721 VMLKKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 721 VMLKKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFFEQMON 770

RESULT 4
AAW40130
ID AAW40130 standard; Protein; 770 AA.
XX
AC AAW40130;
XX
DT 03-JUN-1998 (first entry)
XX
YY Human APP770 protein.

Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiodopathy;
brain; membrane-spanning glycoprotein; beta-amyloid precursor protein;
APP770; chromosome 21; human; Alzheimer's disease; AD; amyloid filament;
treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.

OS Homo sapiens.
XX
PN WO9748983-A1.
XX
PD 24-DEC-1997.
XX
PF 18-JUN-1997; 97WO-US10601.
XX
PR 18-JUN-1996; 96US-0665649.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
PI Citron M, Schenk D, Selkoe DJ, Seubert PA;
XX
DR WPI: 1998-063287/06.
DR N-PSDB; AAV10322.
XX

PT Identifying compounds that alter cellular production of amyloid-beta
PT 42 fragment - in vitro or in transgenic animal models, potentially
PT useful for treatment of Alzheimer's and other amyloid deposition
PT diseases

Disclosure; Fig 10; 86pp; English.

CC This sequence represents the human beta-amyloid precursor protein
CC APP770, which is a membrane-spanning glycoprotein encoded by a gene
CC on the long arm of chromosome 21. A fragment of the APP protein is known
CC as the amyloid-beta peptide (A-beta), also known as the beta-AP peptide,
CC which forms the subunit of the amyloid filaments comprising senile
CC (amyloid) plaques and the amyloid deposits in small cerebral and
CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be
CC a 39-43 amino acid fragment. This invention provides methods of screening
CC compounds for their ability to alter the production of the A-beta
CC peptide, which is composed of >41 amino acids, alone, or in combination
CC with the A-beta peptide composed of 40 amino acids or less. Such agents
CC that reduce the production of the A-beta peptide are potentially useful
CC for treatment of Alzheimer's Disease or other diseases involving amyloid
CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with
CC amyloidosis of Dutch type and advanced aging of the brain.

XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 19; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60

Db 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTK 60
OY 61 TCIDTKEGILQYQYVPELOITNVEANOPVTIQNMCKRGKQCKTHPHFVPIRCLVG 120
Db 61 TCIDTKEGILQYQYVPELOITNVEANOPVTIQNMCKRGKQCKTHPHFVPIRCLVG 120
OY 121 EFVSDALLVPDKCKFLQERMDVCETHLHMHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLQERMDVCETHLHMHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
OY 181 GVEFVCCPLAEESDNDVSADAEEDSDVMMWGADTDYADGSEDKVVEVAEEVEVAEVEE 240
Db 181 GVEFVCCPLAEESDNDVSADAEEDSDVMMWGADTDYADGSEDKVVEVAEEVEVAEVEE 240
OY 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTTTTSVEEVVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTTTTSVEEVVREVCSQAETGPC 300
OY 301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNPDTEEYCMVCGSAMSQSLKTTQEPPLARD 360
Db 301 RAMISRWFVDVTEGKCAPFFYGGCGGNRNPDTEEYCMVCGSAMSQSLKTTQEPPLARD 360
OY 361 PVKLPTTAASPDPAVDKYLETPGDENEHAHFOKAKERLLEAKHREMSQVMREBEAEROA 420
Db 361 PVKLPTTAASPDPAVDKYLETPGDENEHAHFOKAKERLLEAKHREMSQVMREBEAEROA 420
OY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
OY 481 QAVPRPRHVFENMLKRYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVTHLRVIYER 540
Db 481 QAVPRPRHVFENMLKRYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVTHLRVIYER 540
OY 541 MNQSLSLYNVPAVAEEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTET 600
Db 541 MNQSLSLYNVPAVAEEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTET 600
OY 601 KTTVELLPVNGEESLDDLPWHSFGADSVPAANTEVEVPDARPAADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEESLDDLPWHSFGADSVPAANTEVEVPDARPAADRGLTTRPGSGLTN 660
OY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIIGLMGVVIATYIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIIGLMGVVIATYIVITL 720
OY 721 VMLKKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 721 VMLKKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFFEQMON 770

RESULT 5
AAW97996
ID AAW97996 standard; Protein; 770 AA.

XX AAW97996;
AC
XX
DT 21-JUN-1999 (first entry)
XX
DE Human amyloid precursor protein.
XX
KW Amyloid precursor protein; APP; human; gene targeting;
KW homologous recombination; transgenic mouse; transgenic animal;
KW animal model; Alzheimer's disease.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Domain 672..711
FT /note="beta-amyloid domain"
XX
PN WO9909150-A1.

XX 25-FEB-1999.
PD 18-AUG-1997; 97WO-US14507.
XX 18-AUG-1997; 97WO-US14507.
PF 18-AUG-1997; 97WO-US14507.
XX
PR 18-AUG-1997; 97WO-US14507.
XX
PA (FARB) BAYER CORP.
XX
PI WIRAK DO;
XX WPI; 1999-181029/15.
DR
XX Modification of target nucleic acids - by homologous recombination,
PT used particularly for introducing a humanised amyloid precursor
PT protein gene into rodents for producing models of Alzheimer's
PT disease
XX
XX Disclosure; Page 85-88; 209pp; English.
XX
XX This polypeptide comprises human amyloid precursor protein (hAPP).
CC The invention provides a novel gene targeting strategy that
CC facilitates the introduction of one or more specific mutations
CC into any gene in a single double reciprocal homologous recombination
CC step. The method has been used particularly for introducing a
CC humanised APP gene into rodents for producing animal models of
CC Alzheimer's disease (AD). 4 Independent lines of transgenic mice
CC (lines ES5007, ES5103, ES5401 and ES5403) have been created using
CC the novel gene targeting technique applied to embryonic stem cells.
CC In each line, the mouse APP gene was modified to encode a
CC mouse/human hybrid (m/hAPP) where amino acid residues 666-770 of
CC APP770 are encoded by human cDNA sequences instead of mouse genomic
CC exons (exons 16-18). Within these residues, only 3 amino acid
CC differences exist between the mouse and human proteins, i.e.
CC Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. This exon-cDNA
CC fusion gene therefore encodes an APP containing a humanised
CC beta-amyloid domain. Swedish, London, Swedish/London and stop
CC mutations have also been introduced. Targeting vector sequences
CC are provided (see AAX24730-33).
XX
XX Sequence 770 AA;
SQ

Query Match 100.0%; Score 4058; DB 20; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGIALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHNVQNGKWDSPSGTK 60
1 MLPGIALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYQCEVYPELQITNVVEANQPVTIQNWCKRGRCKTHPHFVIRCLVG 120
61 TCIDTKEGILQYQCEVYPELQITNVVEANQPVTIQNWCKRGRCKTHPHFVIRCLVG 120
DB 61 TCIDTKEGILQYQCEVYPELQITNVVEANQPVTIQNWCKRGRCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEETHLHWHVAKETCSEKSTNLADYGMLLPCGIDKFR 180
121 EFVSDALLVPDKCKFLHQERMDVCEETHLHWHVAKETCSEKSTNLADYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCEETHLHWHVAKETCSEKSTNLADYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240
181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240
QY 241 EADDEDDEDGDEVEEAEPEYEAEATERTSIATTTTTTTSVEEYVREVCSQOAEATGPC 300
241 EADDEDDEDGDEVEEAEPEYEAEATERTSIATTTTTTTSVEEYVREVCSQOAEATGPC 300
DB 241 EADDEDDEDGDEVEEAEPEYEAEATERTSIATTTTTTTSVEEYVREVCSQOAEATGPC 300
QY 301 RAMISRMYFDVTEGKCAPFFYGGCGGNRNNEDTTEYCMAYCGSAMQSLLKTTQEPLARD 360
301 RAMISRMYFDVTEGKCAPFFYGGCGGNRNNEDTTEYCMAYCGSAMQSLLKTTQEPLARD 360
DB 301 RAMISRMYFDVTEGKCAPFFYGGCGGNRNNEDTTEYCMAYCGSAMQSLLKTTQEPLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHRRMSQVMREWEAEARQA 420
361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHRRMSQVMREWEAEARQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHRRMSQVMREWEAEARQA 420

QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITAL 480
421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITAL 480
DB 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRVDPKKAQIRSQVMTHLRIYER 540
481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRVDPKKAQIRSQVMTHLRIYER 540
DB 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRVDPKKAQIRSQVMTHLRIYER 540
QY 541 MNQSLSLLYNPVAVAEEIODEVDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
541 MNQSLSLLYNPVAVAEEIODEVDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
DB 541 MNQSLSLLYNPVAVAEEIODEVDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFSLDDIQPMHSFGADSVPANTENEYEPVDARPAADRGTLTRPGSGLTN 660
601 KTTVELLPVNGEFSLDDIQPMHSFGADSVPANTENEYEPVDARPAADRGTLTRPGSGLTN 660
DB 601 KTTVELLPVNGEFSLDDIQPMHSFGADSVPANTENEYEPVDARPAADRGTLTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVIAIVITL 720
661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVIAIVITL 720
DB 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVIAIVITL 720
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEOMON 770
721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEOMON 770
DB 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEOMON 770

RESULT 6
AAE10648
ID AAE10648 standard; Protein; 770 AA.

XX AAE10648;

DT 10-DEC-2001 (first entry)

XX Human amyloid protein precursor 770 (APP770) isoform.

XX Human; aspartyl protease 1; Aspl; amyloid precursor protein 770; APP770;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX Homo sapiens.

PN GB2357767-A.

XX 04-JUL-2001.

XX 22-SEP-2000; 2000GB-0023315.

XX 23-SEP-1999; 99US-0155493.

PR 23-SEP-1999; 99US-0404133.

PR 23-SEP-1999; 99WO-US20881.

PR 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Bienkowski MJ, Gurney M;

DR WPI; 2001-444208/48.

XX N-PSDB; AAD17897.

XX Polyptide comprising fragments of human aspartyl protease with

PT amyloid precursor protein processing activity and alpha-secretase

CC activity, for identifying modulators useful in treating Alzheimer's

CC disease -

PS Example 8; Page 142-144; 187pp; English.

XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified

CC Aspl proteins which lack transmembrane domain or amino terminal

CC domain or cytoplasmic domain and retains alpha-secretase activity

CC and amyloid protein precursor (APP) processing activity. The proteins

CC of the invention are useful for assaying hu-Aspl alpha-secretase

CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is amyloid protein
CC precursor 770 (App770) isoform from human.

XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 22; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNMNMNVONGKWDSPSGTK 60
1 MLEPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNMNMNVONGKWDSPSGTK 60
DB 61 TCIDTKEGILQYCCQEVVPELQITNVEANQPVTIQNMCKRGRKQCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVEVAEEEEVAEEEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVEVAEEEEVAEEEE 240
QY 241 EADDEDEDEGDEVEEEAEPEYEATERTTSIATTTTTSVEVEEVREVCSQAETGPC 300
DB 241 EADDEDEDEGDEVEEEAEPEYEATERTTSIATTTTTSVEVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNFDTEEYCMAYCGSAMSQSLKTQEPRLARD 360
DB 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNFDTEEYCMAYCGSAMSQSLKTQEPRLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAERQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAERQA 420
QY 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVFNMKKYVRAEQKDRQHTLKHFEHVRVNDPKKAQIRSQVMTHLRIYER 540
DB 481 QAVPPRRHVFNMKKYVRAEQKDRQHTLKHFEHVRVNDPKKAQIRSQVMTHLRIYER 540
QY 541 MNQSLSLYNPAPAEEIODEVDELLOKEQNSDVLANMISEPRISYGNDAIMPSLTET 600
DB 541 MNQSLSLYNPAPAEEIODEVDELLOKEQNSDVLANMISEPRISYGNDAIMPSLTET 600
QY 601 KTTVELLPVNGEFSLDLQPMWSFGADSVPAANTENEVEPYDARPADRGLTTRPGSLTN 660
DB 601 KTTVELLPVNGEFSLDLQPMWSFGADSVPAANTENEVEPYDARPADRGLTTRPGSLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVNHQKLVFAEDVGSNKGAILIGLMGVVATIVITL 720
DB 661 IKTEEISEVKMDAEFRHDSGYEVNHQKLVFAEDVGSNKGAILIGLMGVVATIVITL 720
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 770
DB 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 770

RESULT 7
AAE11762
ID AAE11762 standard; Protein; 770 AA.

XX
AC AAE11762;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human amyloid precursor protein (APP).
XX
KW Human; neuroprotective; nootropic; immunostimulant; Alzheimer's disease;
KW anticonvulsant; vaccine; gene therapy; Pick's disease; antidiabetic;
KW systemic amyloidosis; maturity onset diabetes; Parkinson's disease;
KW Huntington's disease; fronto-temporal dementia; encephalopathy; ALS;
KW amyotrophic lateral sclerosis; amyloid precursor protein; APP.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Protein /label= Signal_peptide
FT /label= Mature_human_APP_protein
FT Domain 18..700
FT /label= Extracellular_domain
FT Region 672..714
FT /note= "Abeta-42/43 core peptide"
FT Domain 700..723
FT Region /label= Transmembrane_domain
FT /note= "C-100 fragment"
FT Domain 723..770
FT /label= Intracellular_domain
XX
PD WO200162284-A2.
XX
PD 30-AUG-2001.
XX
PF 19-FEB-2001; 2001WO-DK00113.
XX
PR 21-FEB-2000; 2000DK-0000265.
PR 01-MAR-2000; 2000US-186295P.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Birk P, Jensen MR, Nielsen KG;
XX
DR WPI: 2001-589796/66.
DR N-PSDB; AAD18754.
XX
PT In vivo down-regulation of amyloid protein for the treatment of
PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
PT subsequence and/or at least one analogue of the amyloidogenic
PT polypeptide to the immune system -
XX
PS Claim 23; Page 113-116; 120pp; English.
XX
CC The invention relates to a method for in vivo down-regulation of amyloid
CC protein such as beta amyloid (Abeta) in an animal, including human. The
CC method comprising presenting to the animal's immune system an
CC immunogenically effective amount of at least one amyloidogenic protein
CC or its subsequence and/or at least one analogue of the amyloidogenic
CC polypeptide. The amyloidogenic protein or its subsequence, and its
CC analogue is useful for the preparation of an immunogenic composition
CC comprising an adjuvant for down-regulating amyloid in an animal. They are
CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
CC disease or other diseases characterised by amyloid deposits. They are
CC also useful in the treatment of systemic amyloidosis, maturity onset
CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and
CC prion-related transmissible spongiform encephalopathies. They are also
CC useful for inducing production of antibodies against an amyloidogenic
CC polypeptide. The present sequence is human amyloid precursor protein
CC (APP).
XX
SQ Sequence 770 AA;

Query Match		100.0%;	Score 4058;	DB 22;	Length 770;	
Best Local Similarity		100.0%;	Pred. No. 4.4e-289;			
Matches 770;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	MLPGIALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK	60			
Db	1	MLPGIALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK	60			
QY	61	TCIDTKEGILQYCQEVVPELQITNVVEANQPTIQNWCKRGKQCKTHPHFVIPIRYCLVG	120			
Db	61	TCIDTKEGILQYCQEVVPELQITNVVEANQPTIQNWCKRGKQCKTHPHFVIPIRYCLVG	120			
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180			
Db	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180			
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE	240			
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE	240			
QY	241	EADDDDEDEDGDEVEEEAEPEYEATERTTSIATTTTTTSSVEEVVREVCSQAETGPC	300			
Db	241	EADDDDEDEDGDEVEEEAEPEYEATERTTSIATTTTTTSSVEEVVREVCSQAETGPC	300			
QY	301	RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMQSLLKTQEPLARD	360			
Db	301	RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMQSLLKTQEPLARD	360			
QY	361	PVKLPPTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA	420			
Db	361	PVKLPPTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA	420			
QY	421	KNLPKADKKAIVIQHFQEKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480			
Db	421	KNLPKADKKAIVIQHFQEKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480			
QY	481	QAVPPRRHVFNMKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIYER	540			
Db	481	QAVPPRRHVFNMKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIYER	540			
QY	541	MNQSLLYNVPAVAEEIQDEVDLQKQNSDDVLANMISEPRISYGNDAIMPSTET	600			
Db	541	MNQSLLYNVPAVAEEIQDEVDLQKQNSDDVLANMISEPRISYGNDAIMPSTET	600			
QY	601	KTTVELLPVNGEESLDDLQPMHSFGADSVPAANTENEVEVPDARPAADRGTLTRPGSGLTN	660			
Db	601	KTTVELLPVNGEESLDDLQPMHSFGADSVPAANTENEVEVPDARPAADRGTLTRPGSGLTN	660			
QY	661	IKTEEISEVKMDAEFRHDSGYEVHOKLVFEAEVGSNKGAIIGLMVGGVVIATVITL	720			
Db	661	IKTEEISEVKMDAEFRHDSGYEVHOKLVFEAEVGSNKGAIIGLMVGGVVIATVITL	720			
QY	721	VMLKKQYTSIHGVEVDAAVTPERRHLSKMQONGYENPTYKFEQMQN	770			
Db	721	VMLKKQYTSIHGVEVDAAVTPERRHLSKMQONGYENPTYKFEQMQN	770			
RESULT 8						
ID	AAE06893 standard; Protein; 770 AA.					
XX	AAE06893;					
AC	AAE06893;					
XX	23-OCT-2001 (first entry)					
DT	23-OCT-2001 (first entry)					
DE	Human amyloid precursor protein 770 (APP770) isoform.					
XX	Human; aspartyl protease; beta-amyloid precursor protein 770; APP770;					
KW	beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;					
KW	neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;					
KW	neuroprotective; antisense therapy; gene therapy; chromosome 21.					

OS	Homo sapiens.
XX	
PN	W0200150829-A2.
XX	
PD	19-JUL-2001.
XX	
PF	09-MAY-2001; 2001WO-IB00799.
XX	
PR	09-MAY-2001; 2001WO-IB00799.
XX	
PA	(BIEN/) BIENKOWSKI M J.
PA	(GURN/) GURNEY M E.
PA	(HEIN/) HEINRIKSON R L.
PA	(PARO/) PARODI L A.
XX	(YANR/) YAN R.
PI	Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX	
DR	WPI; 2001-483072/52.
DR	N-PSDB; AAD13278.
XX	
PT	Novel purified polypeptide comprising fragment of mammalian aspartyl
PT	protease 2, lacking Asp2 transmembrane domain and retaining beta
PT	secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT	activity
XX	
PS	Claim 8; Page 171-173; 185pp; English.
XX	
CC	The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC	precursor protein (APP) isoforms and their corresponding DNA molecules.
CC	Human aspartyl proteases can act as beta-secretase proteases useful for
CC	treating Alzheimer's disease. APP isoforms are useful for identifying
CC	modulators of amyloid-beta peptide production, for use in designing
CC	therapeutics for the treatment and prevention of Alzheimer's disease,
CC	dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC	and neuronal loss. APP isoforms are also used in methods for identifying
CC	inhibitors and modulators of human Asp2 activity. The invention relates
CC	to a method for identifying agents that modulate the activity of human
CC	aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC	as a means to screen in cellular assays for the inhibitors of beta- and
CC	gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC	polymerase chain reactions (PCR). The probes are useful for detecting
CC	Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
CC	blots. The present sequence is human wild-type amyloid precursor
CC	protein 770 (APP770) isoform. APP770 gene is localised of chromosome 21.
XX	
SQ	Sequence 770 AA;
Query Match	
Best Local Similarity 100.0%; Score 4058; DB 22; Length 770;	
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLMHNMNVQNGKWDSPSGTK
Db	1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLMHNMNVQNGKWDSPSGTK
QY	61 TCIDTKEGILQYCQEVVPELQITNVVEANQPTIQNWCKRGKQCKTHPHFVIPIRYCLVG
Db	61 TCIDTKEGILQYCQEVVPELQITNVVEANQPTIQNWCKRGKQCKTHPHFVIPIRYCLVG
QY	121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR
Db	121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR
QY	181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE
Db	181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEEVEE
QY	241 EADDDDEDEDGDEVEEEAEPEYEATERTTSIATTTTTTSSVEEVVREVCSQAETGPC
Db	241 EADDDDEDEDGDEVEEEAEPEYEATERTTSIATTTTTTSSVEEVVREVCSQAETGPC
QY	301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMQSLLKTQEPLARD

Db 301 RAMISRMWFDVTEGKCAPFFYGGCGGNRNNFDETEYCMAVCGSAMQSLSLKTQEPRLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Db 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
QY 541 MNQSLSLYNPVPAVAEEIQDEVELLQKEQNSDDVLAMNISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVPAVAEEIQDEVELLQKEQNSDDVLAMNISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGERSLDDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGERSLDDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGVVIATVIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIIGLMVGVVIATVIVITL 720
QY 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEEQMQN 770
Db 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEEQMQN 770

RESULT 9
AAU06622 standard; protein; 770 AA.
ID AAU06622 standard; protein; 770 AA.
XX AAU06622;
XX 24-OCT-2001 (first entry)
DE Human partial Amyloid precursor protein, APP770.
XX Human; Aspartyl protease; Asp2; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KV amyloid-beta; Abeta; APP770.
XX Homo sapiens.
OS

Key Location/Qualifiers
Misc-difference 358 /note= "Encoded by GCC"

XX WO200149098-A2.
XX 12-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00798.
XX 09-MAY-2001; 2001WO-IB00798.
XX 09-MAY-2001; 2001WO-IB00798.
XX (BIEN/) BIENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARO/) PARODI L A.
XX (YANR/) YAN R.
XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
XX WPI: 2001-502549/55.
XX N-PSDB; AAS11549.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
PS Disclosure; Page 171-173; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is human APP770.
XX
SQ Sequence 770 AA;

Query Match 100.0%; Score 4058; DB 22; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHVQNGKWDSDPSGK 60
Db 1 MHPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRNLNMHVQNGKWDSDPSGK 60
QY 61 TCIDTKEGILQYQCEVYPQLQITNVVEANQPVTIQNMCKRGKCKTHPHFVIRCLVG 120
Db 61 TCIDTKEGILQYQCEVYPQLQITNVVEANQPVTIQNMCKRGKCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEHLHWHVAKETCSEKSTNLHDYGLMLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCEHLHWHVAKETCSEKSTNLHDYGLMLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
Db 241 EADDDDEDDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
QY 301 RAMISRMWFDVTEGKCAPFFYGGCGGNRNNFDETEYCMAVCGSAMQSLSLKTQEPRLARD 360
Db 301 RAMISRMWFDVTEGKCAPFFYGGCGGNRNNFDETEYCMAVCGSAMQSLSLKTQEPRLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
Db 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYER 540
QY 541 MNQSLSLYNPVPAVAEEIQDEVELLQKEQNSDDVLAMNISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVPAVAEEIQDEVELLQKEQNSDDVLAMNISEPRISYGNDAIMPSTLET 600

PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-0520881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Bienkowski MJ, Gurney M;
XX
XX
DR MPI; 2001-444208/48.
DR N-PSDB; AAD17899.
XX
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
XX
PS Disclosure; Page 148-151; 187pp; English.

The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
Asp1 proteins which lack transmembrane domain or amino terminal
domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC protein precursor 770-KK (APP770-KK) isoform. APP770-KK isoform is
CC obtained by the addition of two Lys residues (KK motif) at the
CC C-terminal of APP770 protein.
XX
XX
SQ Sequence 772 AA;

Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGIALLLAAWTARALEVPTDGNAGLAEPQIAMEFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGIALLLAAWTARALEVPTDGNAGLAEPQIAMEFCGRLNMHMNVQNGKWDSPSGTK 60
Db 61 TCIDTKEGILQYCOEYVPELQITNVNEANQPYTIQNMCKRGKQCKTHPHVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMHYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMHYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE 240
Db 181 GVEFVCCPLAEESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE 240
QY 241 EADDEDEDEGDEVEEEAEPEYEATERTTSTATTTTTTTSVEEVEVVCSEQAETGPC 300
Db 241 EADDEDEDEGDEVEEEAEPEYEATERTTSTATTTTTTTSVEEVEVVCSEQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPEFYGGCGGNRNPFTEEYCMAYCGSAMSQSLKTTQEPLARD 360
Db 301 RAMISRWYFDVTEGKCAPEFYGGCGGNRNPFTEEYCMAYCGSAMSQSLKTTQEPLARD 360
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHQAKERLEAKHREMSQVWREWEAEARQA 420
Db 361 PVKLPTTAASPDAVDKYLETPGDENEHAHQAKERLEAKHREMSQVWREWEAEARQA 420
QY 421 KNLPKADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480

Db 421 KNLPKADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHRVFNMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIER 540
Db 481 QAVPPRRHRVFNMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNNPVAVAEEIQDEVDDELQEKQNYSDVLANMISEPRISYNDALMPSLTET 600
Db 541 MNQSLSLYNNPVAVAEEIQDEVDDELQEKQNYSDVLANMISEPRISYNDALMPSLTET 600
QY 601 KTTVELLPVNGEESLDDLOPMHSFGADSVPAANTENEVEVPDARPADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEESLDDLOPMHSFGADSVPAANTENEVEVPDARPADRGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGAIIIGLVGVVIAIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGAIIIGLVGVVIAIVITL 720
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
Db 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770

RESULT 12
AAE06895
ID AAE06895 standard; Protein; 772 AA.
XX
AC AAE06895;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human amyloid precursor protein 770-KK (APP770-KK) isoform.
XX
KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 770-KK;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW neuroprotective; antisense therapy; gene therapy; APP770-KK; mutant;
KW mutuin.
XX
XX Homo sapiens.
OS Synthetic.
OS
PN WO200150829-A2.
XX
PD 19-JUL-2001.
XX
PF 09-MAY-2001; 2001WO-IB00799.
XX
PR 09-MAY-2001; 2001WO-IB00799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
PI
XX
DR MPI; 2001-483072/52.
DR N-PSDB; AAD133280.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX
PS Disclosure; Page 177-180; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying

modulators of amyloid-beta peptide production, for use in designing
therapeutics for the treatment and prevention of Alzheimer's disease,
dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
and neuronal loss. App isoforms are also used in methods for identifying
inhibitors and modulators of human Asp2 activity. The invention relates
to a method for identifying agents that modulate the activity of human
aspartyl protease Asp2. Amyloid-beta peptides obtained from App are used
as a means to screen in cellular assays for the inhibitors of beta- and
gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
polymerase chain reactions (PCR). The probes are useful for detecting
Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
blots. The present sequence is modified human amyloid precursor protein
770-KK (APP770-KK) isoform. APP770-KK isoform is obtained by addition of
two Lys residues (KK motif) at the C-terminal end of APP770 isoform.

Sequence 772 AA;

Query Match 100.0%; Score 4058; DB 22; Length 772;

Best Local Similarity 100.0%; Pred. No. 4.4e-289;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLPGALLLLAAWTAARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKMSDPSGK 60
1 MLPGALLLLAAWTAARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKMSDPSGK 60
61 TCIDTKEGILQYCEVYPELQITNVVEANQPTIQNWCKRGKQCKTHPHEVYIPRCLVG 120
61 TCIDTKEGILQYCEVYPELQITNVVEANQPTIQNWCKRGKQCKTHPHEVYIPRCLVG 120
121 EFVSDALVLPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
121 EFVSDALVLPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADGSEDKVEVAEEEAEEVEE 240
181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADGSEDKVEVAEEEAEEVEE 240
241 EADDEDEDEGDEVEEAEPEYEATERTTSTATTTTSTESVEEVREVCSQOETGPC 300
241 EADDEDEDEGDEVEEAEPEYEATERTTSTATTTTSTESVEEVREVCSQOETGPC 300
301 RAMISRWFYDTEGKCAPFEYGGCGGNRNFDTEECMAVCGSAMSQSLKTQDEPLARD 360
301 RAMISRWFYDTEGKCAPFEYGGCGGNRNFDTEECMAVCGSAMSQSLKTQDEPLARD 360
361 PVKLPTTAASTPDADVVKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAEQA 420
361 PVKLPTTAASTPDADVVKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAEQA 420
421 KNLPRADKKAVIQHFEQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYTAL 480
421 KNLPRADKKAVIQHFEQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYTAL 480
481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYIER 540
481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYIER 540
541 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNALMPSLTET 600
541 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNALMPSLTET 600
601 KTTVELLPVNGEFSLDLQPMHSFGADSVPAANTENEVEPYDARPAADRGLTRPGSLTN 660
601 KTTVELLPVNGEFSLDLQPMHSFGADSVPAANTENEVEPYDARPAADRGLTRPGSLTN 660
661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVIAIVITL 720
661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIGLMVGGVIAIVITL 720
721 VMLKKQYTSIHGVVEVDAVTPERHLKMQQNGYENPTYKFEQOMON 770
721 VMLKKQYTSIHGVVEVDAVTPERHLKMQQNGYENPTYKFEQOMON 770

RESULT 13
AAU06624
ID AAU06624 standard; Protein; 772 AA.
AC AAU06624;
DT 24-OCT-2001 (first entry)
DE Human Amyloid precursor protein mutant, APP770-KK.
KW Human; Aspartyl protease; Asp2b; beta-secretase; nootropic;
KW neuroprotective; amyloid protein precursor; App; Alzheimer's disease;
KW amyloid-beta; Abeta; APP770-KK; mutant; mutein.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 358 /note= "Encoded by GCC"
FT Misc-difference 771..772 /note= "2 Extra Lys residues added compared to wild-type APP770"
FT
XX WO200149098-A2.
XX 12-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00798.
XX 09-MAY-2001; 2001WO-IB00798.
XX 09-MAY-2001; 2001WO-IB00798.
XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R:
XX
XX WPI; 2001-502549/55.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
PS Disclosure; Page 177-180; 185pp; English.
XX
CC The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence are methods of identifying
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-Sw-beta-secretase peptide sequence (NMDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridise to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is the human
CC APP770 mutant, APP770-KK which has 2 extra Lys residues added at

CC the C-terminus compared to the wild-type App770. The mutation alters the
CC specificity of the App gamma-secretase activity and increases the rate
CC of processing of the amyloid Abeta peptide.
XX

SO Sequence 772 AA;

Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATEERTTSIATTTTTTTSVEEVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATEERTTSIATTTTTTTSVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNFDTEECMAVCGSAMSQSLKTQEPPLARD 360
Db 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNFDTEECMAVCGSAMSQSLKTQEPPLARD 360
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420
Db 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420
QY 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRVNDPKKAAQIRSQVMTHLYIER 540
Db 481 QAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRVNDPKKAAQIRSQVMTHLYIER 540
QY 541 MNQSLSLYNPVAAVEIQDEYDELLQKEQNSDVLANMISEPRISYGNDAIMPSLTET 600
Db 541 MNQSLSLYNPVAAVEIQDEYDELLQKEQNSDVLANMISEPRISYGNDAIMPSLTET 600
QY 601 KTTVELLPVNGEFSLDLQIPWHSFGADSVPAANTENEVEPYDARPAADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDLQIPWHSFGADSVPAANTENEVEPYDARPAADRGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAILGLMWGVVIAIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAILGLMWGVVIAIVITL 720
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEOMON 770
Db 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEOMON 770

RESULT 14
AAU07223
ID AAU07223 standard; Protein; 772 AA.

XX AAU07223;

DT 24-OCT-2001 (first entry)

DE Human beta-amyloid protein precursor, isoform App770-KK.

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;
KW aspartyl protease 2; Asp2; amyloid protein precursor; App;
KW beta-secretase; Alzheimer's disease; APP770-KK.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Misc-difference 358
FT /note= "Encoded by ggc"

PN MO200149097-A2.

XX 12-JUL-2001.

PF 09-MAY-2001; 2001WO-IB00797.

PR 09-MAY-2001; 2001WO-IB00797.

XX (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.

XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;

DR WPI; 2001-502548/55.

DR N-PSDB; AAS11736.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity

XX Disclosure; Page 177-180; 185pp; English.

XX The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing
CC an APP cleavage site recognisable by a mammalian beta-secretase, and
CC further comprising two lysine residues at the carboxyl terminus of the
CC amino acid sequence of the mammalian APP or APP fragment. The
CC polypeptides are used for assaying for modulators of beta-secretase
CC activity; identifying agents that inhibit the APP processing activity
CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
CC modulate the activity of Asp2; and for reducing cellular production of
CC amyloid beta (Abeta) from APP. Agents identified by the above methods
CC are useful for treating Alzheimer's disease; and for identifying
CC modulators of amyloid-beta (Abeta) peptide production, for use in
CC designing therapeutics for the treatment or prevention of Alzheimer's
CC disease. Probes and primers derived from Asp nucleic acid sequences
CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence represents the amino
CC acid sequence of human amyloid protein precursor, isoform App770-KK,
CC used in the method of the invention.

SO Sequence 772 AA;

Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60

Db 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120

Db 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIPYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
QY 241 EADDEDEDGDEVEEEAEEDYEATERTTSIATTTTTTTSVEEVEVREVCSQAETGPC 300
DB 241 EADDEDEDGDEVEEEAEEDYEATERTTSIATTTTTTTSVEEVEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSAMSQSLKTTQEPRLARD 360
DB 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSAMSQSLKTTQEPRLARD 360
QY 361 PVKLPPTTAATPDVADKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA 420
DB 361 PVKLPPTTAATPDVADKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA 420
QY 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIER 540
DB 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLLYNVPVAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
DB 541 MNQSLLYNVPVAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
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RESULT 15
AAE02602
AAE02602 standard; protein; 772 AA.
AAE02602;
XX 10-AUG-2001 (first entry)
XX Human amyloid precursor protein 770-KK (APP 770-KK) protein.
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 358 /note= "Encoded by GGC"
FT
XX
XX WO200123533-A2.
XX
XX 05-APR-2001.
XX
XX 22-SEP-2000; 2000WO-US26080.
XX
XX 23-SEP-1999; 99US-0155493.
XX 23-SEP-1999; 99WO-US20881.
XX 13-OCT-1999; 99US-0416901.

PR 06-DEC-1999; 99US-0169232.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
XX Gurney M, Bienkowski MJ;
XX
XX WPI; 2001-290516/30.
DR N-PSDB; AAD06772.
DR
XX
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
XX
PS Example 8; Page 176-179; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP 770-KK protein.
XX
SQ Sequence 772 AA;
Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4,4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 TCIDTKEGILQYCCQEVYPELQITNVEANQPVITQNMCKRGKQCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
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QY 241 EADDEDEDGDEVEEEAEEDYEATERTTSIATTTTTTTSVEEVEVREVCSQAETGPC 300
DB 241 EADDEDEDGDEVEEEAEEDYEATERTTSIATTTTTTTSVEEVEVREVCSQAETGPC 300
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DB 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSAMSQSLKTTQEPRLARD 360
QY 361 PVKLPPTTAATPDVADKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA 420
DB 361 PVKLPPTTAATPDVADKYLETGPDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQA 420
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DB 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
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QY 541 MNQSLLYNVPVAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
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QY 661 IKTEETSEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAITGLMVGCVIATVITL 720
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Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFPAEDVGSNKGAIIIGLMVGVIATVITL 720
Oy 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFEOMON 770
Db 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFEOMON 770

Search completed: October 31, 2002, 10:11:59
Job time : 57.9852 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 20.8364 Seconds
(without alignments)
902.637 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLAAMTARALEV.....KMQONGYENPTYKFFEQMON 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4058	100.0	770	1 US-08-133-248-8	Sequence 8, Appli
2	4058	100.0	770	1 US-08-231-940-1	Sequence 1, Appli
3	4058	100.0	770	2 US-08-641-774-1	Sequence 1, Appli
4	4058	100.0	770	2 US-08-104-165-3	Sequence 3, Appli
5	4058	100.0	770	3 US-08-464-250-3	Sequence 3, Appli
6	4058	100.0	770	4 US-08-464-250-3	Sequence 3, Appli
7	3943.5	97.2	751	1 US-08-123-702-4	Sequence 4, Appli
8	3943.5	97.2	751	2 US-08-104-165-2	Sequence 2, Appli
9	3943.5	97.2	751	2 US-08-422-333-2	Sequence 2, Appli
10	3943.5	97.2	751	2 US-08-422-333-21	Sequence 21, Appli
11	3943.5	97.2	751	3 US-08-464-250-2	Sequence 2, Appli
12	3943.5	97.2	751	4 US-08-464-250-2	Sequence 2, Appli
13	3943.5	97.2	751	6 5187153-2	Patent No. 5187153
14	3943.5	97.2	751	6 5223482-2	Patent No. 5223482
15	3937.5	97.0	751	6 5220013-2	Patent No. 5220013
16	3590.5	88.5	695	1 US-08-123-702-2	Sequence 2, Appli
17	3590.5	88.5	695	2 US-08-104-165-1	Sequence 1, Appli
18	3590.5	88.5	695	3 US-08-464-250-1	Sequence 1, Appli
19	3590.5	88.5	695	4 US-08-464-250-1	Sequence 1, Appli
20	3590.5	88.5	695	4 US-09-458-481B-7	Sequence 7, Appli
21	3590.5	88.5	695	4 US-09-458-481B-8	Sequence 8, Appli
22	3590.5	88.5	695	6 5218100-2	Patent No. 5218100
23	3584.5	88.3	694	1 US-08-339-152A-18	Sequence 18, Appli
24	3584.5	88.3	694	2 US-08-007-999B-5	Sequence 5, Appli
25	3584.5	88.3	694	2 US-08-689-276A-5	Sequence 5, Appli
26	3578.5	88.2	695	1 US-08-371-930-27	Sequence 27, Appli
27	3578.5	88.2	695	5 PCT-US94-01712-27	Sequence 27, Appli

28	3566.5	87.9	695	1 US-08-339-152A-30	Sequence 30, Appli
29	3493.5	86.1	695	4 US-09-458-481B-6	Sequence 6, Appli
30	3489.5	86.0	695	4 US-09-458-481B-4	Sequence 4, Appli
31	3471.5	85.5	676	1 US-08-371-930-24	Sequence 24, Appli
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33	3468.5	85.5	695	4 US-09-458-481B-5	Sequence 5, Appli
34	3366.5	83.0	656	1 US-08-371-930-23	Sequence 23, Appli
35	3366.5	83.0	656	5 PCT-US94-01712-23	Sequence 23, Appli
36	3356.5	82.7	1024	4 US-09-522-666-2	Sequence 2, Appli
37	2393.5	59.0	487	1 US-08-462-859A-9	Sequence 9, Appli
38	2393.5	59.0	487	1 US-08-123-659A-9	Sequence 9, Appli
39	2393.5	59.0	487	1 US-08-464-247A-9	Sequence 9, Appli
40	2393.5	59.0	487	1 US-08-464-248A-9	Sequence 9, Appli
41	2393.5	59.0	492	1 US-08-462-859A-7	Sequence 7, Appli
42	2393.5	59.0	492	1 US-08-123-659A-7	Sequence 7, Appli
43	2393.5	59.0	492	1 US-08-464-247A-7	Sequence 7, Appli
44	2393.5	59.0	492	1 US-08-464-248A-7	Sequence 7, Appli
45	1975.5	48.7	763	1 US-08-155-331-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1									
US-08-133-248-8									
; Sequence 8, Application US/08133248									
; Patent No. 5525714									
; GENERAL INFORMATION:									
; APPLICANT:									
; TITLE OF INVENTION: MUTATED FORM OF THE BETA-AMYLOID PRECURSOR									
; TITLE OF INVENTION: PROTEIN GENE									
; NUMBER OF SEQUENCES: 8									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/133,248									
; INFORMATION FOR SEQ ID NO: 8:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 770 amino acids									
; TYPE: amino acid									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
US-08-133-248-8									
Query Match 100.0%; Score 4058; DB 1; Length 770;									
Best Local Similarity 100.0%; Pred. No. 5.8e-281;									
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MLPGLALLLAAMTARALEVPTDGNAGLAEPOIAMFCGRNMHNMVQNGKWDSPSGTK	60						
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QY	61	TCIDTKEGILQYCOEVPYPELQITNVVEANQPVTIQNMCKRGRKQCKTHPHFVIRCLVG	120						
DB	61	TCIDTKEGILQYCOEVPYPELQITNVVEANQPVTIQNMCKRGRKQCKTHPHFVIRCLVG	120						
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR	180						
DB	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR	180						
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE	240						
DB	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE	240						
QY	241	EADDEDDEDGDEVEEAEPEYEATERTTSIATTTTTSVEVEVREVCSQAETGPC	300						
DB	241	EADDEDDEDGDEVEEAEPEYEATERTTSIATTTTTSVEVEVREVCSQAETGPC	300						
QY	301	RAMISRWFVDVTEGKCAPFFYGGCGGNRNFDTTEYCMVCGSAMQSLSLKTTOEPLARD	360						

Db 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEECMAVCGSAMQSLSLKTQOEPLARD 360
QY 361 PVKLPTASTPDADVVKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
Db 361 PVKLPTASTPDADVVKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
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Db 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
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RESULT 2

US-08-231-940-1
; Sequence 1, Application US/08231940
; Patent No. 5550216
; GENERAL INFORMATION:
; APPLICANT: MIYAZAKI, Kaoru
; TITLE OF INVENTION: GELATINASE A INHIBITOR
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,940
; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-120457
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-62129
; FILING DATE: 08-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NEIMARK, Sheridan
; REGISTRATION NUMBER: 20,520
; REFERENCE/DOCKET NUMBER: MIYAZAKI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-231-940-1

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLAEPQIAMFCGRNLNMHMYQNGKWDSDPSGK 60
Db 1 MLPGALLLLAAWTARALEVPTDGNAGLAEPQIAMFCGRNLNMHMYQNGKWDSDPSGK 60
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Db 61 TCIDTKEGILQYCOEYVPELOITNVNEANQPVTIQNWCKRGKQCKTHPHFVIPIYRCLVG 120
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QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEECMAVCGSAMQSLSLKTQOEPLARD 360
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Db 361 PVKLPTASTPDADVVKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEAEERQA 420
QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
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QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFFEQMON 770
Db 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFFEQMON 770

RESULT 3

US-08-641-774-1
; Sequence 1, Application US/08641774
; Patent No. 5843695
; GENERAL INFORMATION:
; APPLICANT: MIYAZAKI, Kaoru
; TITLE OF INVENTION: BETA-AP DECOMPOSING AGENT
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,774
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,474
FILING DATE: 25-APR-1994
APPLICATION NUMBER: JP 5-122207
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-51133
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: MIYAZAKI-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-641-774-1

Query Match 100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60
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Db 61 TCIDTKEGILQYCOEVYPELQITNVVEANOPVTIQNWCKRGRKOCKTHPHFVIRCLVG 120
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Db 121 EEVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGADTDYADGSEDKVVEAAEEVEAEVEEE 240
Db 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGADTDYADGSEDKVVEAAEEVEAEVEEE 240
QY 241 EADDDDEDEDGEVEEAEPEEATERRTSIATTTTTTTSVEEVREVCSQAETGPC 300
Db 241 EADDDDEDEDGEVEEAEPEEATERRTSIATTTTTTTSVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGNRNNFDTEECMAVCGSAMSQSLKTQEPPLARD 360
Db 301 RAMISRWYFDVTEGKCAPFFYGGCGNRNNFDTEECMAVCGSAMSQSLKTQEPPLARD 360
QY 361 PVKLEPTTAASPDADVKKYLETPGDENENAHFQKAKERLEAKHREMSQVMREWEAEARQA 420
Db 361 PVKLEPTTAASPDADVKKYLETPGDENENAHFQKAKERLEAKHREMSQVMREWEAEARQA 420
QY 421 KNLPRADKKAVIQHFQEKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRADKKAVIQHFQEKVESLEGEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKHEHVRMVDPKKAAQIRSQVMTHLRVIER 540

Db 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKHEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVAAVEEIQDEVELLQKEQNSDVLAMNISEPRISYGNALMBSLET 600
Db 541 MNQSLSLYNPVAAVEEIQDEVELLQKEQNSDVLAMNISEPRISYGNALMBSLET 600
QY 601 KTVLELLPVNGEFSLDDIQPMHSFGADSVPAANTENEVEPVADARPADRGLTTRPSGLTN 660
Db 601 KTVLELLPVNGEFSLDDIQPMHSFGADSVPAANTENEVEPVADARPADRGLTTRPSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAIVITL 720
QY 721 VMLKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFEOMON 770
Db 721 VMLKKQYTSIHGVEYDAVTPPEERHLSKMQONGYENPTYKFEOMON 770

RESULT 4
US-08-104-165-3
Sequence 3, Application US/08104165
Patent No. 5877015

GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Alison Mary
APPLICANT: MULLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-3

Query Match 100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60

|||||
Db 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVEANQPTVIONWCKRGKQCKTHPHFVPIPYRCLVG 120
Db 61 TCIDTKEGILQYCEVYPELOITNVEANQPTVIONWCKRGKQCKTHPHFVPIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTEYCMVCGSAMSQSLKTTQEPPLARD 360
Db 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTEYCMVCGSAMSQSLKTTQEPPLARD 360
QY 361 PVKLPTTAASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVWREWEAEARQA 420
Db 361 PVKLPTTAASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVWREWEAEARQA 420
QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
Db 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVAAEIQDEVEDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVAAEIQDEVEDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFSLDLQPMWHSFGADSVRPANTENEVEPVDARPAADRGTLTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDLQPMWHSFGADSVRPANTENEVEPVDARPAADRGTLTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGVIATVIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGVIATVIVITL 720
QY 721 VMLKKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
Db 721 VMLKKKQYTSIHGVEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770

RESULT 5
US-08-464-250-3
; Sequence 3, Application US/08464250
; Patent No. 6107542
; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; APPLICANT: GOATE, Alison Mary
; APPLICANT: MULLAN, Michael John
; APPLICANT: CHARTIER-HARLIN, Marie-Christine
; APPLICANT: OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-250-3

Query Match 100.0%; Score 4058; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVEANQPTVIONWCKRGKQCKTHPHFVPIPYRCLVG 120
Db 61 TCIDTKEGILQYCEVYPELOITNVEANQPTVIONWCKRGKQCKTHPHFVPIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTEYCMVCGSAMSQSLKTTQEPPLARD 360
Db 301 RAMISRWFYDVTGKCAFFYGGCGGNRNFDTEYCMVCGSAMSQSLKTTQEPPLARD 360
QY 361 PVKLPTTAASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVWREWEAEARQA 420
Db 361 PVKLPTTAASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVWREWEAEARQA 420
QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
Db 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVAAEIQDEVEDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVAAEIQDEVEDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600

QY 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEYVDARPAADRGLTTRPGSLTN 660
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Db 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEYVDARPAADRGLTTRPGSLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMGCVIATVIYITL 720
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Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMGCVIATVIYITL 720
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
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Db 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
RESULT 6
US-08-464-250-3
; Sequence 3, Application US/08464250
; Patent No. 6300540
; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; GOATE, Alison Mary
; MULLAN, Michael John
; CHARTIER-HARLIN, Marie-Christine
; OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,250
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/104,165
; FILING DATE: 21-JAN-1992
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-464-250-3
Query Match 100.0%; Score 4058; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNVQNGKWDSPSGTK 60
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Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVNEANQPTIQNWCCKRGKCKCKTHPHFVIRCLVG 120

Db 61 TCIDTKEGILQYCEVYPELOITNVNEANQPTIQNWCCKRGKCKCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
|||||
Db 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVEVAEEEAEEVEE 240
|||||
Db 181 GVEFVCCPLAEESDNVDSADAEEEDSDVWVGADTDYADGSEDKVEVAEEEAEEVEE 240
QY 241 EADDDDEDEDGEVEEAEEPEYEATERTTSIATTTTTTESVEEVVREVCSEQAETGPC 300
|||||
Db 241 EADDDDEDEDGEVEEAEEPEYEATERTTSIATTTTTTESVEEVVREVCSEQAETGPC 300
QY 301 RAMISRWFYDTEGKCAFFYGGCGGNRNNFDTEECMAVCGSAMSOSLKTTOEPLARD 360
|||||
Db 301 RAMISRWFYDTEGKCAFFYGGCGGNRNNFDTEECMAVCGSAMSOSLKTTOEPLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVREWEAEARQA 420
|||||
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHRERMSQVREWEAEARQA 420
QY 421 KNLPRADKKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
|||||
Db 421 KNLPRADKKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMYDPKKAQIRSQVMTLRYIER 540
|||||
Db 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMYDPKKAQIRSQVMTLRYIER 540
QY 541 MNOSLSLLYNPVAVEETODEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSETET 600
|||||
Db 541 MNOSLSLLYNPVAVEETODEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSETET 600
QY 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEYVDARPAADRGLTTRPGSLTN 660
|||||
Db 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEYVDARPAADRGLTTRPGSLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMGCVIATVIYITL 720
|||||
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMGCVIATVIYITL 720
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
|||||
Db 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOQNGYENPTYKFFEQMON 770
RESULT 7
US-08-123-702-4
; Sequence 4, Application US/08123702
; Patent No. 5604131
; GENERAL INFORMATION:
; APPLICANT: Wadsworth, Samuel
; APPLICANT: Snyder, Benjamin
; APPLICANT: Reddy, Vermuril, B.
; APPLICANT: Wei, Chamer
; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding App770
; Patent No. 5604131
; TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,702
FILING DATE: 17-SEPT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TSII121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-702-4

Query Match 97.2%; Score 3943.5; DB 1; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAAEEEAEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAAEEEAEEVEE 240
QY 241 EADDEDEDEGDEVEEAEEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
Db 241 EADDEDEDEGDEVEEAEEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNFTTEYCAVCSAMSQSLKTQEPFLARD 360
Db 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNFTTEYCAVCSAMSQSLKTQEPFLARD 360
QY 361 PVKLPPTTAASPDAVKYLETGPDENEHAHFQAKERLEAKHREMSQVMREMEAEARQA 420
Db 345 ---IPTTAASPDAVKYLETGPDENEHAHFQAKERLEAKHREMSQVMREMEAEARQA 401
QY 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQOLVETTHMARVEAMLNDRRLALENYITAL 480
Db 402 KNLPRADKKAVIQHFOEKVESLEQEAANERQOLVETTHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHYRMVDPKKAQIRSQVMTHLRIYER 540
Db 462 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHYRMVDPKKAQIRSQVMTHLRIYER 521
QY 541 MNQSLSLYNPAAVEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTER 600
Db 522 MNQSLSLYNPAAVEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTER 581
QY 601 KTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDARPAADRGLTRPGSGLTN 660
Db 582 KTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDARPAADRGLTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMVGVIATVIVITL 720
Db 642 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMVGVIATVIVITL 701
QY 721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 770

Db 702 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 751

RESULT 8
US-08-104-165-2
Sequence 2, Application US/08104165
Patent No. 5877015
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Alison Mary
APPLICANT: MULLEN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-2

Query Match 97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAAEEEAEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAAEEEAEEVEE 240
QY 241 EADDEDEDEGDEVEEAEEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300

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Db 241 EADDEDEDEGEVEEEAEPEYEAEATERTSIATTTTSTESVEEVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRRNFDTEEYCAVCGSAMSQSLKTTOEPLARD 360
Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRRNFDTEEYCAVCGSA----- 344
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQA 420
Db 345 ---IPTTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQA 401
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 402 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKFHEHVRAVDPKKAAQIRSQVMTHLRYIER 540
Db 462 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKFHEHVRAVDPKKAAQIRSQVMTHLRYIER 521
QY 541 MNQSLSLLYNVPAAVEEIQDEYDELLQKEQNYSSDVLANMISEPRISYNDALMPSLTET 600
Db 522 MNQSLSLLYNVPAAVEEIQDEYDELLQKEQNYSSDVLANMISEPRISYNDALMPSLTET 581
QY 601 KTTVELLPVNGEFLDLOPWHSGADSVRPANTENEVEPYDARPAADRGLTTRPGSGLTN 660
Db 582 KTTVELLPVNGEFLDLOPWHSGADSVRPANTENEVEPYDARPAADRGLTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGVIATVIYITL 720
Db 642 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGVIATVIYITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 751

RESULT 9
US-08-422-333-2
; Sequence 2, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-422-333-2

Query Match 97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPLGLALLLAAWTARALEVPTDGNAGLLAEPLQIAMFCGRMLNMHNVQNGKWDSDPSGTR 60
Db 1 MLPLGLALLLAAWTARALEVPTDGNAGLLAEPLQIAMFCGRMLNMHNVQNGKWDSDPSGTR 60
QY 61 TCIDTKEGILQYCCQEVYPELQITNVEANQPVITQNMCKRGKQCKTHPHFVIRPCLVG 120
Db 61 TCIDTKEGILQYCCQEVYPELQITNVEANQPVITQNMCKRGKQCKTHPHFVIRPCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVAEEEEVAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVAEEEEVAEVEE 240
QY 241 EADDEDEDEDEGEVEEEAEPEYEAEATERTSIATTTTSTESVEEVREVCSQAETGPC 300
Db 241 EADDEDEDEDEGEVEEEAEPEYEAEATERTSIATTTTSTESVEEVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRRNFDTEEYCAVCGSAMSQSLKTTOEPLARD 360
Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRRNFDTEEYCAVCGSA----- 344
QY 361 PVKLPTTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQA 420
Db 345 ---IPTTAASPDAVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQA 401
QY 421 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 402 KNLPRKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKFHEHVRAVDPKKAAQIRSQVMTHLRYIER 540
Db 462 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKFHEHVRAVDPKKAAQIRSQVMTHLRYIER 521
QY 541 MNQSLSLLYNVPAAVEEIQDEYDELLQKEQNYSSDVLANMISEPRISYNDALMPSLTET 600
Db 522 MNQSLSLLYNVPAAVEEIQDEYDELLQKEQNYSSDVLANMISEPRISYNDALMPSLTET 581
QY 601 KTTVELLPVNGEFLDLOPWHSGADSVRPANTENEVEPYDARPAADRGLTTRPGSGLTN 660
Db 582 KTTVELLPVNGEFLDLOPWHSGADSVRPANTENEVEPYDARPAADRGLTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGVIATVIYITL 720
Db 642 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGGVIATVIYITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 751

RESULT 10
US-08-422-333-21
; Sequence 21, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View

STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-422-333-21

Query Match 97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKQCKTHPHFVIPYRCLVG 120
Db 61 TCIDTKEGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKQCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHMTYAKETCSEKSTNLHDYGMILPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHMTYAKETCSEKSTNLHDYGMILPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNYSDADAEDSDVWVGADTDYADGSEDKVEVAEEVEAAVEEE 240
Db 181 GVEFVCCPLAEESDNYSDADAEDSDVWVGADTDYADGSEDKVEVAEEVEAAVEEE 240
QY 241 EADDEDDEDEGEVEEAEEPEYEATERTTSTATTTTTSVEEVREVCSEQAETGPC 300
Db 241 EADDEDDEDEGEVEEAEEPEYEATERTTSTATTTTTSVEEVREVCSEQAETGPC 300
QY 301 RAMISRMVFDVTEGKCAFEFFYGCGGNRNNEPTEEXCMAVCGSAMSQSLKTQEPPLARD 360
Db 301 RAMISRMVFDVTEGKCAFEFFYGCGGNRNNEPTEEXCMAVCGSAMSQSLKTQEPPLARD 360
QY 361 PVKLPTASTPDAVDKYLETPGDENEHAHFQAKERLLEAKHREMSQVMREWEAERQA 420
Db 361 PVKLPTASTPDAVDKYLETPGDENEHAHFQAKERLLEAKHREMSQVMREWEAERQA 420
QY 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVFENMLKTYRAEQKDRQHTLKHFEHVMVDPKKAQIRSQVMTHLRYIER 540
Db 481 QAVPRPRHVFENMLKTYRAEQKDRQHTLKHFEHVMVDPKKAQIRSQVMTHLRYIER 540
QY 541 MNQSLSLYVPAVAEEIODEVELQEKQNSDDVLANMISEPRISYGNDALMPSLTET 600
Db 541 MNQSLSLYVPAVAEEIODEVELQEKQNSDDVLANMISEPRISYGNDALMPSLTET 600
QY 601 KTTVELLPVNGEFSLDDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 660

Db 582 KTTVELLPVNGEFSLDDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMGVVATVIVITL 720
Db 642 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMGVVATVIVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 751

RESULT 11

US-08-464-250-2
Sequence 2, Application US/08464250
Patent No. 6107542
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Alison Mary
APPLICANT: MULLEN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-250-2

Query Match 97.2%; Score 3943.5; DB 3; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKQCKTHPHFVIPYRCLVG 120
Db 61 TCIDTKEGILQYCEVYPELQITNVVEANQPVTIQNMCKRGKQCKTHPHFVIPYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
181 GVEFVCCPLAEEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 420
361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 420
Db 345 ---IPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 401
421 KNLPRADKKAVIDHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
402 KNLPRADKKAVIDHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
462 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 521
Db 541 MNQSLLYNVPAAVEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 600
522 MNQSLLYNVPAAVEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 581
QY 601 KTVELLPVNGEESLDDLOPWHSEFADSVRPANTENEVEPVADARPAADRGLTTRPGSGLTN 660
582 KTVELLPVNGEESLDDLOPWHSEFADSVRPANTENEVEPVADARPAADRGLTTRPGSGLTN 641
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAITGLMVGCVIATVITL 720
642 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAITGLMVGCVIATVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPERHLSKMQONGYENPTYKFEQMON 770
702 VMLKKQYTSIHGVEVDAVTPERHLSKMQONGYENPTYKFEQMON 751
Db

RESULT 12
US-08-464-250-2

Sequence 2, Application US/08464250
Patent No. 6300540

GENERAL INFORMATION:

APPLICANT: HARDY, John Anthony

GOATE, Alison Mary

MULLAN, Michael John

CHARTIER-HARLIN, Marie-Christine

OWEN, Michael John

TITLE OF INVENTION: Test and Model for Alzheimer's Disease

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464, 250

FILING DATE: 05-Jun-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-464-250-2
Query Match 97.2%; Score 3943.5; DB 4; length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;
QY 1 MLEPGALLLLAATARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
1 MLEPGALLLLAATARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
Db 1 MLEPGALLLLAATARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTREGILOCYQOEVPPELQITNVEANOPVTIQNWCKRGKQCKTHPHFVIPIRYCLVG 120
61 TCIDTREGILOCYQOEVPPELQITNVEANOPVTIQNWCKRGKQCKTHPHFVIPIRYCLVG 120
Db 61 TCIDTREGILOCYQOEVPPELQITNVEANOPVTIQNWCKRGKQCKTHPHFVIPIRYCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
181 GVEFVCCPLAEEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
Db 181 GVEFVCCPLAEEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTTTSIATTTTTTSEVEEVREVCSQAETGPC 300
QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNFDTEEYCMAYCGSA----- 344
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 420
361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 420
Db 345 ---IPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA 401
421 KNLPRADKKAVIDHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
402 KNLPRADKKAVIDHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
462 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 521
Db 541 MNQSLLYNVPAAVEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 600
522 MNQSLLYNVPAAVEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 581
QY 601 KTVELLPVNGEESLDDLOPWHSEFADSVRPANTENEVEPVADARPAADRGLTTRPGSGLTN 660
582 KTVELLPVNGEESLDDLOPWHSEFADSVRPANTENEVEPVADARPAADRGLTTRPGSGLTN 641
Db 582 KTVELLPVNGEESLDDLOPWHSEFADSVRPANTENEVEPVADARPAADRGLTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAITGLMVGCVIATVITL 720
661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAITGLMVGCVIATVITL 720
Db

Db 642 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMGCVIATVITL 701

QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 770

Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 751

RESULT 13

5187153-2

; Patent No. 5187153

; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO

; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S

; AMYLOID POLYPEPTIDE DERIVATIVES

; NUMBER OF SEQUENCES: 33

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/502,273

; FILING DATE: 29-MAR-1990

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 361,912

; FILING DATE: 06-JUN-1989

; APPLICATION NUMBER: 359,911

; FILING DATE: 12-MAY-1989

; APPLICATION NUMBER: 87,002

; FILING DATE: 18-AUG-1987

; APPLICATION NUMBER: 8,810

; FILING DATE: 30-JAN-1987

; APPLICATION NUMBER: 948,376

; FILING DATE: 31-DEC-1986

; APPLICATION NUMBER: 932,193

; FILING DATE: 17-NOV-1986

; SEQ ID NO:2:

; LENGTH: 751

5187153-2

Query Match 97.2%; Score 3943.5; DB 6; Length 751;

Best Local Similarity 97.4%; Pred. No. 8e-273;

Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLEPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60

Db 1 MLEPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIQNMCKRGRKOCKTHPHFVIRCLVG 120

Db 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIQNMCKRGRKOCKTHPHFVIRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240

Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240

QY 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTTESVEEVVREVCSQAETGPC 300

Db 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTTESVEEVVREVCSQAETGPC 300

QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPRLARD 360

Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPRLARD 360

QY 361 PVKLPFTAASPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420

Db 361 PVKLPFTAASPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420

QY 421 KNLPRADKKAIVIOHFOEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480

Db 421 KNLPRADKKAIVIOHFOEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480

QY 481 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVVRMVDPRKAAQIRSQVMTLRLVIER 540

Db 481 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVVRMVDPRKAAQIRSQVMTLRLVIER 540

QY 462 QAVPRPRHVENMLKKYVRAEQKROHTLKHFEHVVRMVDPRKAAQIRSQVMTLRLVIER 521

QY 541 MNQSLLLYNVPAVAEEIQDEVELLOKEQONYSDDVLAMTISEPRISYGDALMPSLTET 600

Db 522 MNQSLLLYNVPAVAEEIQDEVELLOKEQONYSDDVLAMTISEPRISYGDALMPSLTET 581

QY 601 KTYVELLPVNGEESLDDLOPWHSGADSVPANTENEVEPYDARPAADRGLTRPGSGLTN 660

Db 582 KTYVELLPVNGEESLDDLOPWHSGADSVPANTENEVEPYDARPAADRGLTRPGSGLTN 641

QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMGCVIATVITL 720

Db 642 IKTEEISEVKMDAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMGCVIATVITL 701

QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 770

Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 751

RESULT 14

5223482-2

; Patent No. 5223482

; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL, BARBARA

; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE

; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE

; NUMBER OF SEQUENCES: 34

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/361,912

; FILING DATE: 06-JUN-1989

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 359,911

; FILING DATE: 12-MAY-1989

; APPLICATION NUMBER: 87,002

; FILING DATE: 18-AUG-1987

; APPLICATION NUMBER: 8,810

; FILING DATE: 30-JAN-1987

; APPLICATION NUMBER: 948,376

; FILING DATE: 31-DEC-1986

; APPLICATION NUMBER: 932,193

; FILING DATE: 17-NOV-1986

; SEQ ID NO:2:

; LENGTH: 751

5223482-2

Query Match 97.2%; Score 3943.5; DB 6; Length 751;

Best Local Similarity 97.4%; Pred. No. 8e-273;

Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLEPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60

Db 1 MLEPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIQNMCKRGRKOCKTHPHFVIRCLVG 120

Db 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIQNMCKRGRKOCKTHPHFVIRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240

Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEVEEE 240

QY 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTTESVEEVVREVCSQAETGPC 300

Db 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTTESVEEVVREVCSQAETGPC 300

QY 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPRLARD 360

Db 301 RAMISRWFYDVTGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPRLARD 360

QY 361 PVKLPFTAASPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420

Db 345 ---IPPTAASPPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVREWEAEARQA 401
QY 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 480
Db 402 KNLPRADKKAIVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 461
QY 481 QAVPPRRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYER 540
Db 462 QAVPPRRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYER 521
QY 541 MNQSLSLYNPVPAVAEEIODEVEDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 522 MNQSLSLYNPVPAVAEEIODEVEDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTLET 581
QY 601 KTTVELLPVNGEESLDDLQPMHSEFGADSVPANTENEVEPVDAARPADRGLTTRPGSGLTN 660
Db 582 KTTVELLPVNGEESLDDLQPMHSEFGADSVPANTENEVEPVDAARPADRGLTTRPGSGLTN 641
QY 661 IKTEEISEYKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGVIAIVITL 720
Db 642 IKTEEISEYKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGVIAIVITL 701
QY -721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEOMON 770
Db 702 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEOMON 751

RESULT 15
5220013-2
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:2:
; LENGTH: 751
; 5220013-2

Query Match 97.0%; Score 3937.5; DB 6; Length 751;
Best Local Similarity 97.1%; Pred. No. 2.1e-272;
Matches 748; Conservative 3; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPOIAMFCGRLNMHMNVONGKWDSDPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPOIAMFCGRLNMHMNVONGKWDSDPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVNEANQPTVIONWCKRGKQCKTHPHFVIRYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVNEANQPTVIONWCKRGKQCKTHPHFVIRYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEE 240
QY 241 EADDEDEDEGDEVEEEAEPEYEATERTSIATTTTTSVEEVRVVCSEQAETGPC 300
Db 241 EADDEDEDEGDEVEEEAEPEYEATERTSIATTTTTSVEEVRVVCSEQAETGPC 300

Db 241 EADDEDEDEGDEVEEEAEPEYEATERTSIATTTTTSVEEVRVVCSEQAETGPC 300
QY 301 RAMISRMVFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMQSOLKTTQOPLARD 360
Db 301 RAMISRMVFDVTEGKCAPFFYGGCGGNRNNDTEEYCMVCGSAMQSOLKTTQOPLARD 344
QY 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVREWEAEARQA 420
Db 345 ---IPPTAASPPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVREWEAEARQA 401
QY 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 480
Db 402 KNLPRADKKAIVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 461
QY 481 QAVPPRRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYER 540
Db 462 QAVPPRRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYER 521
QY 541 MNQSLSLYNPVPAVAEEIODEVEDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 522 MNQSLSLYNPVPAVAEEIODEVEDELLOKEQNSDDVLANMISEPRISYGNDAIMPSTLET 581
QY 601 KTTVELLPVNGEESLDDLQPMHSEFGADSVPANTENEVEPVDAARPADRGLTTRPGSGLTN 660
Db 582 KTTVELLPVNGEESLDDLQPMHSEFGADSVPANTENEVEPVDAARPADRGLTTRPGSGLTN 641
QY 661 IKTEEISEYKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGVIAIVITL 720
Db 642 IKTEEISEYKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLVGVIAIVITL 701
QY 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEOMON 770
Db 702 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEOMON 751

Search completed: October 31, 2002, 10:13:33
Job time : 24.8364 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 30.3075 Seconds
(without alignments)
2441.270 Million cell updates/sec

Title: US-09-785-215-2

Perfect score: 4058

Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMON 770

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4058	100.0	770	1	QRHUA4	Alzheimer's disease
2	3590.5	88.5	695	1	A49795	Alzheimer's disease
3	3493.5	86.1	695	2	S00550	Alzheimer's disease
4	3468.5	85.5	695	2	A27485	Alzheimer's disease
5	3403.5	83.9	747	2	JH0773	Alzheimer's disease
6	2446.5	60.3	484	4	A32761	hypothetical Alzhe
7	1981.5	48.8	763	2	A49321	amyloid beta (A4)
8	1971.5	48.6	765	2	S42880	amyloid precursor-
9	1956.5	48.2	751	2	A49974	beta-amyloid precu
10	1150.5	28.4	653	2	A46362	amyloid precursor-
11	1112.5	27.4	511	2	JC1404	CDEI-box DNA-bindi
12	785	19.3	686	2	T15795	hypothetical prote
13	737.5	18.2	886	2	A32758	beta-amyloid-like
14	706	17.4	246	2	S38344	CDEI-binding prote
15	501	12.3	100	2	A32282	Alzheimer's disease
16	411	10.1	82	2	PQ0438	Alzheimer's disease
17	403	9.9	76	2	S06678	Alzheimer's disease
18	397	9.8	76	2	S03607	Alzheimer's disease
19	383	9.4	76	2	S04855	Alzheimer's disease
20	296.5	7.3	191	2	A35981	Alzheimer's disease
21	283	7.0	57	2	E60045	sperm membrane pro
22	283	7.0	57	2	F60045	Alzheimer's disease
23	283	7.0	57	2	G60045	Alzheimer's disease
24	283	7.0	57	2	D60045	Alzheimer's disease
25	283	7.0	57	2	A60045	Alzheimer's disease
26	283	7.0	57	2	B60045	Alzheimer's disease
27	256.5	6.3	111	2	S41082	amyloid precursor
28	217	5.3	42	2	PN0512	beta-amyloid prote
29	194.5	4.8	2225	2	T26063	hypothetical prote

30	186	4.6	993	2	S49461	synaptonemal compl
31	183.5	4.5	396	2	S53325	tissue factor path
32	183	4.5	1188	2	T46608	zinc finger protei
33	179.5	4.4	1208	2	T27822	hypothetical prote
34	178.5	4.4	1110	2	I51116	NF-180 - sea lamp
35	177.5	4.4	2167	2	T34395	hypothetical prote
36	176.5	4.3	252	2	JG0185	hepatocyte growth
37	176	4.3	55	2	S30332	proteinase inhibit
38	175.5	4.3	579	2	JH0820	160K golgi antigen
39	175	4.3	302	1	T1RTGK	tissue factor path
40	175	4.3	1182	2	T30189	myelin transcripti
41	174.5	4.3	1271	2	A45555	glutamate rich pro
42	173.5	4.3	1087	2	T30330	gelsolin-related p
43	173.5	4.3	1558	2	C89114	protein C37C3.6a l
44	172	4.2	922	2	T23573	hypothetical prote
45	170.5	4.2	5170	2	T15348	hypothetical prote

ALIGNMENTS

RESULT 1
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inl
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasci
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288,'V',365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A>Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-p
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simil
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: NID:g178863; PIDN:AAA51768.1; PID:g178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, J
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 87, 257-263, 1990
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A;Reference number: I39451; MUID:90236318
 A;Accession: I39452
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A;Molecule type: DNA
 A;Residues: 1-770 <YOS1>
 A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A;Accession: I39451
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A;Molecule type: DNA
 A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
 A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A;Reference number: A59020; MUID:91340168
 A;Contents: annotation; erratum
 A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A;Reference number: I39453; MUID:90260663
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A;Reference number: I59562; MUID:92022553
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 689-716,'F',718-737 <MUR>
 A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R;Kamino, K.; Orr, H.T.; Payaml, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A;Reference number: A44017; MUID:93035397
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692,'G',694-718 <KAM1>
 A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
 A;Experimental source: familial Alzheimer disease family LT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
 A;Reference number: A03134; MUID:87144572
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288,'V',365-770 <KAN>
 A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A;Note: alternative splice form APP(695)
 R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
 A;Reference number: A29030; MUID:87231971
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
 A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A;Note: the authors translated the codon GAG for residue 647 as Asp

R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A;Reference number: A47584; MUID:87120328
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756,'S',758-770 <GOL>
 A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A;Reference number: A47585; MUID:87120329
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
 A;Reference number: S02638; MUID:88296437
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DYR>
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
 A;Reference number: S00707; MUID:88122640
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344,'I',365-366 <TAN2>
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
 A;Reference number: S00925; MUID:88122639
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344,'I',365-770 <PO2>
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A;Reference number: A38949; MUID:88122641
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288,'V',365-770 <VIT1>
 A;Accession: B30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 122-288,'V',365-770 <VIT2>
 A;Accession: C30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 606-770 <VIT3>
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A;Reference number: A31087; MUID:88124954

A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R: Masters, C.L.; Muthaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.5e-210;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDPKEGILQYCOEVYPELQITNVVEANQPTIQNMCKRGKCKTHPHFVIPYRCLVG 120
Db 61 TCIDPKEGILQYCOEVYPELQITNVVEANQPTIQNMCKRGKCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWMGGADTDYADGSEDKVVEVAEEVEAEVEEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWMGGADTDYADGSEDKVVEVAEEVEAEVEEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
QY 301 RAMISRMVFDYTEGKCAPEFYGGCGGNRNFDTTEYCMVCGSAMSQSLKTQOEPLARD 360
Db 301 RAMISRMVFDYTEGKCAPEFYGGCGGNRNFDTTEYCMVCGSAMSQSLKTQOEPLARD 360
QY 361 PVKLPPTTAATPDVADKYLETPGDENEHAHFQAKERLEAKHRRMSQVREWEAEERQA 420
Db 361 PVKLPPTTAATPDVADKYLETPGDENEHAHFQAKERLEAKHRRMSQVREWEAEERQA 420
QY 421 KNLPRADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 540
Db 481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLAMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLAMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEPVDAADRGGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEPVDAADRGGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIATVIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIATVIVITL 720
QY 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFEQMQN 770
Db 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFEQMQN 770

RESULT 2
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins
C:Keywords: alternative splicing

Query Match 88.5%; Score 3590.5; DB 1; Length 695;
Best Local Similarity 90.1%; Pred. No. 6.2e-185;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDPKEGILQYCOEVYPELQITNVVEANQPTIQNMCKRGKCKTHPHFVIPYRCLVG 120
Db 61 TCIDPKEGILQYCOEVYPELQITNVVEANQPTIQNMCKRGKCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWMGGADTDYADGSEDKVVEVAEEVEAEVEEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWMGGADTDYADGSEDKVVEVAEEVEAEVEEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEYVREVCSQAETGPC 300
QY 301 RAMISRMVFDYTEGKCAPEFYGGCGGNRNFDTTEYCMVCGSAMSQSLKTQOEPLARD 360
Db 289 ----- 288
QY 361 PVKLPPTTAATPDVADKYLETPGDENEHAHFQAKERLEAKHRRMSQVREWEAEERQA 420
Db 289 ---VPTTAATPDVADKYLETPGDENEHAHFQAKERLEAKHRRMSQVREWEAEERQA 345
QY 421 KNLPRADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 346 KNLPRADKKAIVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 405
QY 481 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 540
Db 406 QAVPRPRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 465
QY 541 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLAMISEPRISYGNDAIMPSTLET 600
Db 466 MNQSLSLYNPVAVAEIQDEVELLQKEQNSDDVLAMISEPRISYGNDAIMPSTLET 525
QY 601 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEPVDAADRGGLTTRPGSGLTN 660
Db 526 KTTVELLPVNGEFSLDDLPWHSFGADSVPAANTENEVEPVDAADRGGLTTRPGSGLTN 585
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIATVIVITL 720
Db 586 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIATVIVITL 645
QY 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFEQMQN 770
Db 646 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQNGYENPTYKFEQMQN 695

RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A;Reference number: S00550; MUID:88312583
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
JBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitors; alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 86.1%; Score 3493.5; DB 2; Length 695;
Best Local Similarity 87.7%; Pred. No. 9.7e-180;
Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTVRALEVPDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQVPTIQNMCKRGKQCKTHPHFVTPYRCLVG 120
Db 61 TCIGTKEGILQYCOEYVPELOITNVVEANQVPTIQNMCKRGKQCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEEVEE 240
Db 181 GVEFVCCPLAEESDSIDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEVREVCSEQAETGPC 300
Db 241 EAEDDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEVREVCSEQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGNRNFDTEEYCMVCGSAMQSLLKTQEPPLARD 360
Db 289 ----- 288
QY 361 PVKLPPTASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQA 420
Db 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRRMSQVMREWEAEARQA 345
QY 421 KNLPKADKKAIVQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
Db 346 KNLPKADKKAIVQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405

QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 540
Db 406 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRVIER 465
QY 541 MNQSLILYNPAVAEEIQDEVELLOKEQNYSDVLANMISEPRISYGNDAIMPSTLET 600
Db 466 MNQSLILYNPAVAEEIQDEVELLOKEQNYSDVLANMISEPRISYGNDAIMPSTLET 525
QY 601 KTTVELLPVNGEESLDDLQPMHSEGADSVPAENTENEVEVPDARPAADRGTLTPGSGLTN 660
Db 526 KTTVELLPVNGEESLDDLQPMHSEGVDSVPANTENEVEVPDARPAADRGTLTPGSGLTN 585
QY 661 IKTEEISEVKMDAEFRHDSGEVYHHQKLVFAEDVGSNKGAITGLMVGCVIATVITL 720
Db 586 IKTEEISEVKMDAEFGHDSGEVYHHQKLVFAEDVGSNKGAITGLMVGCVIATVITL 645
QY 721 VMLKKOYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 646 VMLKKOYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A;Reference number: A27485; MUID:88106489
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closely related to the human amyloid beta protein precursor
A;Reference number: S19727; MUID:92096458
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitors; alternative splicing; amyloid; transmembrane protein
A;Accession: I49485
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics: 16C3
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitors; alternative splicing; amyloid; transmembrane protein
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 85.5%; Score 3468.5; DB 2; Length 695;
Best Local Similarity 87.3%; Pred. No. 2.1e-178;
Matches 672; Conservative 6; Mismatches 17; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTVRALEVPDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQVPTIQNMCKRGKQCKTHPHFVTPYRCLVG 120
Db 61 TCIGTKEGILQYCOEYVPELOITNVVEANQVPTIQNMCKRGKQCKTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

|||||
Db 121 EFVSDALVDPCKFLHQERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAEVEE 240
Db 181 GVEFVCCPLAESDSDSADAEEDSDVWVGADTDYADGEDKVVEVAEEEEVAEVEE 240
QY 241 EADDEDDEDEGEVEEAEPEYEATERTTSIATTTTTTESVEEVREVCSQAETGPC 300
Db 241 EADDEDDEDEGEVEEAEPEYEATERTTSTATTTTTTESVEEVV----- 288
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLKTQEP LARD 360
Db 289 ----- 288
QY 361 PVKLPPTASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420
Db 289 ---VPTTASTPDADVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 345
QY 421 KNLPRADKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 346 KNLPRADKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 405
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRYIER 540
Db 406 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKATQIRSQVMTLRYIER 465
QY 541 MNQSLSLYNPAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTET 600
Db 466 MNQSLSLYNPAVAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTET 525
QY 601 KTTVELLPVNGEESLDDLQPMHSGADSVAPANTENEVEVPDARPAADRGITTRPGSGLTN 660
Db 526 KTTVELLPVNGEESLDDLQPMHSGADSVAPANTENEVEVPDARPAADRGITTRPGSGLTN 585
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAITGLMGVVIATVIVITL 720
Db 586 IKTEEISEVKMDAEFGHDSGFEVRHQKLVFAEDVGSNKGAITGLMGVVIATVIVITL 645
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 646 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 5

JH0773

Alzheimer's disease amyloid beta protein precursor - African clawed frog
Species: Xenopus laevis (African clawed frog)
Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
Accession: JH0773
Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
Reference number: JH0773; MUID:93129227
Accession: JH0773
Molecule type: mRNA
Residues: 1-747 <OKA>
Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
Experimental source: larva
Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match

Best Local Similarity 83.9%; Score 3403.5; DB 2; Length 747;
Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

QY 17 ALEVPTDGNAGLAEPQIAME-CGR LNMHMNVQNGKWDSPSGTKTCTIDTKEGILQYCE 75
Db 15 ALEVLDGNGGLAEPOIAMFSVARLNMHMNVQNGKMETDVSG--CIGTKEGILQYCE 71
QY 76 VPELOITNVVEANQPTIQQWCKRGKQCKTHPHFVPIYRCLVGEFVS DALLVPDKCKF 135
|||||

Db 72 VPELOITNVVEANQPTIQQWCKRGKQCKSRTHIVVPYRCLVGEFVS DALLVPDKCKF 131
QY 136 LHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFRGVEFVCCPLAESDN 195
Db 132 LHOERMDICETHLHMTVAKESCESEKSMLEHYGMLLPCGIDKFRGVEFVCCPSAESES 191
QY 196 VDSADAEEDSDVWVGADTDYADGSEDKVVEVA--EEEVAVEVEEADDEDDEDEGE 253
Db 192 FDSADAEEDSDVWVGADADYDRSDDKAVEAQPDEEEVEVEEETDDED--DGDE 249
QY 254 VEEAEPEYEATERTTSIATTTTTTESVEEVREVCSQAETGPCRAMISRWFVYTE 313
Db 250 AEEPEPEYEATERTTSIATTTTTTESVEEVREVCSQAETGPCRAMISRWFVYTE 309
QY 314 GKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLKTQEP LARDPVKLPPTASTPD 373
Db 310 SKCAQFIYGGCGGNRNFDSDDYCMVCGSV-----IPATAASTPD 350
QY 374 AVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPRADKAVIQ 433
Db 351 AVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPRADKAVIQ 410
QY 434 HFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVENM 493
Db 411 HFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVENM 470
QY 494 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRYIERMNQSLSLYNPA 553
Db 471 LKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRYIERMNQSLSLYNPA 530
QY 554 VAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEE 613
Db 531 VAEIQDEVELLQKEQNSDDVLANMISEPRISYGNDALMPSLTETKTTVELLPVNGEE 590
QY 614 SLDDLQPMHSGADSVAPANTENEVEVPDARPAADRGITTRPGSGLTNIKTEEISEVKMDA 673
Db 591 NIEDLQPMHSGADSVAPANTENEVEVPDARPAADRGITTRPGSGLTNIKTEEISEVKMDS 650
QY 674 EFRHDSGYEVHHQKLVFAEDVGSNKGAITGLMGVVIATVIVITLVMKKKQYTSIH 733
Db 651 EYRHDTAYEVHHQKLVFAEVEGSGNKGAITGLMGVVIATVIVITLVMKKKQYTTIH 710
QY 734 GVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 711 GVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 747

RESULT 6

A32761

hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human
Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
Accession: A32761
Ride Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted
Reference number: A32761; MUID:89346754
Accession: A32761
Molecule type: mRNA
Residues: 1-484 <DES>
Cross-references: GB:M28373
Note: the authors translated the codon ATG for residue 433 as Ieu
Comment: This is the hypothetical translation of a sequence believed to contain cl

Query Match

Best Local Similarity 60.3%; Score 2446.5; DB 4; Length 484;
Matches 463; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 80 LQITNVVEANQPTIQQWCKRGKQCKTHPHFVPIYRCLVGEFVS DALLVPDKCKFLHOE 139
Db 1 LQITNVVEANQPTIQQWCKRGKQCKTHPHFVPIYRCLVGEFVS DALLVPDKCKFLHOE 60
|||||

QY 140 RMDVCEHLHWHVAKETCSEKSTNLHDYGLPCGIDKFRGVEFVCCPIAEESDNVDSA 199
Db 61 RMDVCEHLHWHVAKETCSEKSTNLHDYGLPCGIDKFRGVEFVCCPIAEESDNVDSA 120
QY 200 DAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEAEEEDDEDDEDGEVEEEAE 259
Db 121 DAEEDSDVMWGADTDYADGSEDKVVEVAEEVEEAEEEDDEDDEDGEVEEEAE 180
QY 260 EPEEATERSTATTSTTTSTESVEEVREVCSEQAETGPCRAMISRWFVDTGKCAPF 319
Db 181 EPEEATERSTATTSTTTSTESVEEVREVCSEQAETGPCRAMISRWFVDTGKCAPF 240
QY 320 FYGGCGGNRNNDTEEYCMVCGSAMSQSLKTTQEPPLARDPVKLPPTAASDPDAVDKYL 379
Db 241 FYGGCGGNRNNDTEEYCMVCGSA-----IPTTAASDPDAVDKYL 281
QY 380 ETPGDENEHAFQAKERLEAKHRRMSQVWRWEAEERQAKNLPKADKKAVIOHFOEKV 439
Db 282 ETPGDENEHAFQAKERLEAKHRRMSQVWRWEAEERQAKNLPKADKKAVIOHFOEKV 341
QY 440 ESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVENMLKKYVR 499
Db 342 ESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVENMLKKYVR 401
QY 500 AEOKDRQHTLKHEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNPAVAEEIQ 559
Db 402 AEOKDRQHTLKHEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNPAVAEEIQ 461
QY 560 DEV 562
Db 462 DEV 464

RESULT 7

A49321
amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDEI-binding protein
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49321; S34644; S40519
R:Spischer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Foster, B.
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A:Reference number: A49321; MUID:93250009
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
C:Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131199)
A>Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R:Von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDEI binding protein is an amyloid pred
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <VON>
A:Cross-references: EMBL:Z22572; NID:g394763; PIDN:CAA80295.1; PID:g394764
R:Wasco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:g450391; PIDN:AAC41701.1; PID:g450392
C:Genetics:
A:Gene: GDB:APLP2; APPL2
A:Cross-references: GDB:139159; OMIM:104776
A:Map position: 11q23-11q25

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.8%; Score 1981.5; DB 2; Length 763;
Best Local Similarity 50.4%; Pred. No. 1e-98;
Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

QY 5 LALLLAATARALEV-----PTDGAG--LLAEQIAMFCGRIMHNVQNGKWDSDP 56
Db 15 LLLLLVGLTAPALALAGYIEALANAGTGFAVAEPQIAMFCGRIMHNVNQTGKWEPPD 74
QY 57 SGTKTCIDTKEGILQYCOEVPPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVIPYR 116
Db 75 TGTSCFETKEEVLQYCOEMYPELQITNVMEANORVSIIDWCRRDKQCKS--RFVTPFK 132
QY 117 CLVGEFVSDDLVPDKCKFLHQERMDVCEHLHWHVAKETCSEKSTNLHDYGLPCGI 176
Db 133 CLVGEFVSDDLVPDKCKFLHQERMDVCEHLHWHVAKETCSEKSTNLHDYGLPCGI 192
QY 177 DKFRGVEFVCCPIAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEVEAE 236
Db 193 DQFHGTEFVCCPIAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEVAEEVEAE 245
QY 237 VEE--EEA--DDDEDEDGEVEEEAE-----EPEEATERSTATTSTTTSTESVE 284
Db 246 LEDFTEAVIDEDEDDEEVEEVEDRDYDFTFKGDYNE--ENPTPGSDGTMSDKEIT 303
QY 285 EVVREVCSEQAETGPCRAMISRWFVDTGKCAPFYYGGCGGNRNNDTEEYCMVCGSA 344
Db 304 HDVKAVCSQEAETGPCRAMISRWFVDTGKCAPFYYGGCGGNRNNDTEEYCMVCGSA 363
QY 345 MSQSLKTTQEPPLARDPVKLPPTAASDPDAVDKYLETPGDENEHAFQAKERLEAKHRE 404
Db 364 I-----PPTPLPT-----NDVDVYFETSDADNEHAFQAKERLEAKHRE 403
QY 405 RMSQVWRWEAEERQAKNLPKADKKAVIOHFOEKVESTLEQEAANERQOLVETHMARVEAM 464
Db 404 RMDRVKMEWEAEERQAKNLPKAEQRTLIQHFQAMVKALEKEASEKQOLVETHLARVEAM 463
QY 465 LNDRRRLALENYITALQAVPRPRHVENMLKKYVRAEQKDRQHTLKHEHVRMVDPKKAA 524
Db 464 LNDRRRLALENYITALQAVPRPRHVENMLKKYVRAEQKDRQHTLKHEHVRMVDPKKAA 523
QY 525 QIRSQVMTHLRVIERMNSLSLLYNPAVAEEIQDEVELLOKEQNYSDVLANMISEP 584
Db 524 QIRSQVMTHLRVIERMNSLSLLYNPAVAEEIQDEVELLOKEQNYSDVLANMISEP 572
QY 585 RISYGDALMPSLTETKTVELLPVNGEESLDDLPWHSFGADSVAPANTENEVEVPDAR 644
Db 573 -----DQFTASISETPDVDR---VSSEES-EIIPPHF--HPEPALPENE---DTQP 616
QY 645 AADRGLTTPRGSGLTN----IKTEE--ISEVKMDAEFRHDSGYEVHOKLVFFAEVVG 696
Db 617 ELYHBM--KKSGVGEGDGLGAEKEKVINSKNKVDENMVIDETLDV--KEMIFNAERVG 672
QY 697 S-----NKGALIGLMVGVVIATVIVITLVMLKKKQYTSIHGVVEVD 739
Db 673 GLEERRESVGLREDFSLSSSALIGLLVIAVAIATVIVISLVMLKKRQYGTISHGIVEVD 732
QY 740 AAVTPPEERHLKMQQNGYENPTYKFFEQMO 769
Db 733 PMLTPEERHLKMQQNGYENPTYKFFEQMO 762

RESULT 8

S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994

QY 643 RPADRGITRRPGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFAEDVGS----- 697
Db 613 ----GSGMAEDQG-GLIGAEKVINSKNMNDENMVIDETLDV--KEMIFNAERVGLLEE 665
QY 698 -----NKGAIIGLMVGCVIATVIVITLMLKKQYTSIHGVEVDAVTP 744
Db 666 PESVGPLREDFSLSSNALIGLVIAVAIVIVISLVMLRKQYGTISHGIVEVDPMLTP 725
QY 745 EERHLSKMOQNGYENPTYKFFEQM 769
Db 726 EERHLNKMQNHGYNPTYKYLEQM 750

RESULT 10
A46362
amyloid precursor-like protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
Accession: A46362

Jasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alz
A:Reference number: A46362; MUID:93066322
A:Accession: A46362
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-653 <WAS>
A:Experimental source: brain
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:118683, NCBI:118684)
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: transmembrane protein

Query Match 28.4%; Score 1150.5; DB 2; Length 653;
Best Local Similarity 35.4%; Pred. No. 2.7e-54;
Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

QY 1 MLPGLALLLAAWTARA-LEVPTDGNAGLLAEPOIAMFCGRLNMHNVQNGKWDSPSGT 59
Db 22 LLP-LSLLILRAQLAVGNLAVGSPSAAEAPGSAQVAGLCGLTLHRLDRTGRWEPDQRS 80
QY 60 KTCIDITKEGILQYQEVYPELQITNVVEANQPTIQNMCKRGKQCKTHPHF-VIPYRCL 118
Db 81 RRCLLDPOVLEYCRQMPRELHIAVRAQAIEMERWCGSTRSGRCAHPHHEVVPFHL 140
QY 119 VGEFVSDALLVPDKCKFLHQRMDVCEETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDK 178
Db 141 PGEFVSEALLVPEGCRFLHQRMDCESTRRHQEAQACSSQGLIHSGMLLPCGSDR 200
QY 179 FRGVEEVCPLAEESDNVDSADAEDSDVW-WGADTDYADGSEDKVVEVAEEEA 237
Db 201 FRGVEYVCCP-PRATPNPSGMAAGDSTRSWPLGR---AEGGED-----EEVESEF 248
QY 238 EEEEADEDEDDEDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCSQAET 297
Db 249 PQPVDDYFVERPQAEVEEVEEERAPPPSSHTP----- 281
QY 298 GPCRAMISRMYFDVTEGKCAFFFYGGCGGNRNNDTEEYCAVCGSAMSQSLKTQEPL 357
Db 282 ----VMYSR---VT----- 288
QY 358 ARDPYKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAE 417
Db 289 ---PTPRPT-----DGVDPYFEGMGEIGEHEGFLRAKMDLEERRMQINEVMREMAAD 339
QY 418 RQAKNLEPKADKAVIOHFQEKVESLQEAANERQQLVETHMARVEAMLNDRRLALENYI 477
Db 340 SQSKNLEPKADKQALNHFQESLQLEEQVSGERQRLVETHTATRYALINDQRRALLEGFL 399
QY 478 TALQAVPRPRRHVENMLKKYVRAEQDKRQHTLKHFEHVAVDPKKAQIRSQVMTHLRYI 537
Db 400 AALQGDPPQAEVRLMALRRYLRAEQEKQRHTLRLHYQHVAAVDPKKAQOQMRFOVQTHLOYI 459

QY 538 YERMNQSLLYNVPAVAEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDAIMP-S 596
Db 460 EERMNQSLLGDQNPFLAQELRPQIOELL-----LAEHIGPSEL---DASVPGS 505
QY 597 LLETKTVELLPVNGEFLSDLOPMHSGADSVPAANTENEVEVPDARPAADRGITRRPGS 656
Db 506 SSEDK-----GSLQP-----PESKDDEPVTLP---KGSTDQESS 536
QY 657 GLTNKTEIESEVKMDAEFRHDSGYEVHH--QKLVFAEDVGSNKGAIIGLMVGCVIA 713
Db 537 SSGREKLPLEQYEQKVNASAPRGFPFHSSDIQDELAPSGTGVSRREALSGLLIMGAGG 596
QY 714 TVIVITLVML-KKKQYTSIHGVEVDAVTPPEERHLSKMOQNGYENPTYKFFEQ 767
Db 597 SLIVSLLLLRKKKPYGTISHGVEVDPMLTLLEEQLRELQRHGYNPTYRFLFE 651

RESULT 11
JC1404
CDEI-box DNA-binding protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C:Accession: JC1404
R;Vidal, F.; Biangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
A:Title: A murine sequence-specific DNA binding protein shows extensive local similar
A:Reference number: JC1404; MUID:93129193
A:Accession: JC1404
A:Molecule type: mRNA
A:Residues: 1-511 <VID>
C:Comment: This protein plays an important role in the early development of the mouse
C:Keywords: DNA binding; transmembrane protein

Query Match 27.4%; Score 1112.5; DB 2; Length 511;
Best Local Similarity 43.0%; Pred. No. 2.2e-52;
Matches 264; Conservative 87; Mismatches 136; Indels 127; Gaps 21;

QY 174 CGIDKFRGVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEE 233
Db 6 CGVDQFHGTEYVCCP---QTKYVDS-----DSTMK-----EEEE 37
QY 234 VAEVEEADDEDEDDEDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVREVCS 293
Db 38 ---EEDDEDEEDYDLKSEFTFADLDEFTF---AADEEEDDEEGEVED---- 86
QY 294 QAEIGPCRAMISRMYFDVTEGKCAFFFYGGCGGNRNNDTEEYCAVCGSAMSQSLKTT 353
Db 87 -----RDYYD-----PF---KGDDYNEENPTE-----PSSEGTI--S 114
QY 354 QEPLARDPVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREW 413
Db 115 DKEIVHD-VKVPPTPLPTND-VDYFFETSADDNEHARQAKAQLEIRHRNMRDVKKEW 172
QY 414 EEAERQAKNLPKADKAVIOHFQEKVESLQEAANERQQLVETHMARVEAMLNDRRLAL 473
Db 173 EEAELQAKNLPKTERQTLQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLAL 232
QY 474 ENYITALQAVPRPRRHVENMLKKYVRAEQDKRQHTLKHFEHVAVDPKKAQIRSQVMT 533
Db 233 ENYLAALQSDPRPRPHRILQALRRYVRAENKDRLLHTIRHYQHVLAVDPEKAAQMSQVMT 292
QY 534 LRVIERMNSLSLLYNVPAVAEEIODEVDELLOKEQNYSDVLANMISEPRISYGNDA 593
Db 293 LRVIERMNSLSLLYKVPYVAQEIQEBIDELLOEQR-----ADM-----DOF 335
QY 594 MBSLETKTVELLPVNGEFLSDLOPMHSGADSVPAANTENEVEVPDARPAADRGITTR 653
Db 336 TSSISENPVDVRSSESE-EIPPFHPLHPF---PSISENE-----GSGMAEQ 379
QY 654 PGSGLTNIKTEEI-SEVKMDAEFRHDSGYEVHHQKLVFAEDVGS----- 697
Db 380 DG-GLIGAEKVINSKNMNDENMVIDETLDV--KEMIFNAERVGLLEEPESVGPLREDF 436


```

QY 238 EE-EEADDDDEDEDGDEVEEEAEPEEYA-TERTSIATTTTTTSTESVEEVREVCSEQA 295
      : |||: ||| | | | | | : : : : : | : :
Db 297 DSGEGDNVEEDGAGSESEAEVEASWDSGAKVSVLSKSDSSSPSAPAPAPEKAPVK 356
QY 296 ETGPCRAMISRWFYFDVTGKCAPFFYGCGGNRNNPDTEYCMAVCGSAMQSLLKTQE 355
      | : | : | | | | | | | : : : : : | : :
Db 357 ESVTSPQLS-----ASAATAFVANSGNSGT-----GAGAPPSTAQPTSD 396
QY 356 PLARDPVKLPTTAASTPDAVDKIETPGDENEHAHFOKAKERLEAKHREMSOVMREEE 415
      | | | | | | | | | | | : : : : : | : :
Db 397 P-----YFTHPDHYEHOSYKVSQKRLESHEKREKYTRVMKDWD 435
QY 416 AEROAKNLPKADKA-----VI0HFOEKVESLEOEANERQOLVETHMARVEAMLND 468
      | : : : | | | | : | | : : : | | : | | | |
Db 436 LEEKYODMRLADPKAAQSFQRMTAREQTSVQALEEGNAEKHQLAAMHOQRYLAHNOR 495
QY 469 RRIALENYTALQAVPRPRRHVENMLKKYVRAEQDKDRHTLKHFH-VRMVDP--KKA 524
      : | : | | | | | | | | | | | | | : | :
Db 496 KREAMTCYTQALTQOPRNAHHEKCLCKILRALHKDRAHALAHYRHLLNSGGPGLLEAA 555
      : | : | | | | | | | | | | | | | : | :
    525 QIRSOVMTHLRVIYERMNOSLSLYNPVAVAEI-----QDEV----- 562
Db 556 SERPRTLERLIDIDRAVNQSMTMLKRIPELSAKIAQLMDYILALRSKDIPIGSSLGME 615
QY 563 -----DELLOKEONYSDDVLAN 579
      : | : : | : | : | : | : | : | :
Db 616 EAEGILDKYRVEIERKVAEKERLRLAEKQRAERAEREKLREELKLEAKKVDDLKS 675
QY 580 MISE-----PRISYNDALM-----PSLTETKTVELLPVNG 611
      : : | : : | : : | : | : | : | : | :
Db 676 QVAEQSQOPTQOSTQSOAQOQQQEKSLPGKELGPDALLVTAANPNLETFS----- 726
QY 612 EFSLDLQPMHSFGADSVPAANTENEVEBYDARPAADRGLTRPGSGLTNIKTEEISEVKM 671
      | | | : : | : | | | | | | | : : :
Db 727 EKDLSDTE---YGEATVSTTKVGYVLEPYDDDAVQRAVEDVAAA-----VAHQEA 773
QY 672 DAERHDSCGEVHHQKLVF----FAEDVGSNK---GAIGLMVGCVIATIVITLVML 723
      : : : : : : : | : : : : | : : : : :
Db 774 EPVOYOHFWTHDLGHRESSFSLRREFAOHAHAAKEGRNVYFTLSFAGIALMAAVFVGAVA 833
QY 724 KKQOTSIH-HGVEEVDAAVTP-----EERHLSKMOQNGYENPTYKFFE 766
      | : | | | : | | | | | : : : | | | | | |
Db 834 KWRTSRSPHAOGFIEVDONVTTHPIVBEKIVPNMQINGYENPTYKFFE 883

```

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
Species: Mus musculus (house mouse)
Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996
C/Accession: S38344
R/Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A/Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A/Reference number: S38344; MUID:94032480
A/Accession: S38344
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-246 <HAN>
A/Cross-references: EMBL:Z22592
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

```
Query Match      17.4%; Score 706; DB 2; Length 246;  
Best Local Similarity 51.5%; Pred. No. 5.1e-31;  
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;  
  
QY    5 LALLLLAAMTARALEV-----PTDGNAG---LLAEPOIAMFCGRLLMHMNVQNGKWDSDP 56  
      | : ||| | | | : ||| : ||||| | | : ||| : | | | : ||  
Db    15 LLVLLLLGLTAPAAALAGYTEALANAGTGFAVAEPQIAMLCKLNMHVNIQTGKWEPDP 74  
  
QY    57 SGTCTCIDTKEGILQYCQEVEYPELOITNVEANOPTVIQNCKRGKKQCKTHPHFVIPYR 116  
      : ||| : | | : ||||| : ||||| : ||||| | : || : | : ||| : | ||| :  
Db    75 TGTSCSLGTKEEVLQYCQEIEYPELOITNVEANOPTVIDSWCRDKRKCKS--HIVIPFK 132
```

```
QY 117 CLVGEFVS DALLVPDKCKFLHÖERM DVCETHLHWH TAVAKETCS EKSTNLHDYGM LLLPGCI 176
    ||||| ||||| : : ||||| : || : ||||| :
Db 133 CLVGEFVS DVLVLPDNCQFFHÖERMEVCEKHÖRWH TLVKEACLTEGLTLYSYGMLLPCGV 192
QY 177 DKFRGV EFCPLAEESDNVDSADA EEDSDVWVGADTDYADGS EDKVV EYAE EEEV AE 236
    || : || : ||||| : : ||||| : |||||
Db 193 DQFHGTEVCCP---QTKTVDS-----DSTMSKEEEE--- 222
QY 237 VEEEEADDDDED-DGDGEVEEEAE 259
    || : || : || : || : || :
Db 223 -EEDEDEDEEDYDLDKSEFPTEAD 245
```

```

RESULT 15
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 13-Aug-1999
C/Accession: A32282
R;Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A;Title: Structure and expression of the alternatively-spliced forms of mRNA for the
A;Reference number: A32282; MUID:89149813
A;Accession: A32282
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <YAM>
A;Cross-references: GB:M24397; NID:g200350; PIDN:AAA39929.1; PID:g200351
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing
F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          12.3%; Score 501; DB 2; Length 100;
Best Local Similarity 92.0%; Pred. No. 1.6e-20;
Matches 92; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 281 ESVEEVREVCSQAETGPCRAMISRMYFDVTEGKCAFFYGGCGGNRNNFDTEEYCMAY 340
|||||
|||||
Db 1 ESVEEVREVCSQAETGPCRAMISRMYFDVTEGKCVFFYGGCGGNRNNFDTEEYCMAY 60
|||||
|||||

QY 341 CGSAMSOSILKTTQEPPLARDPVKLPPTAASPDAVDKYLE 380
|||||
|||||
Db 61 CGSVSTQSLKTTSEPLPQDDPKLPPTAASPDAVDKYLE 100
|||||
|||||

```

Search completed: October 31, 2002, 10:13:05
Job time : 36.3075 secs

Gencore version 5.1.3
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OW protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 17.048 seconds
(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2

Perfect score: 4058

Sequence: 1 MDPGLALLLAATARALEV.....KMQQNGYENPTYKFEQMQN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4058	100.0	770	1	A4_HUMAN	P05067 homo sapien
2	3937	97.0	770	1	A4_RAT	P08592 rattus norv
3	3927	96.8	770	1	A4_MOUSE	P12023 mus musculu
4	3921.5	96.6	751	1	A4_SAIISC	Q95241 salmirl sci
5	1981.5	48.8	763	1	APP2_HUMAN	Q06481 homo sapien
6	1971.5	48.6	765	1	APP2_RAT	P15943 rattus norv
7	1704.5	42.0	695	1	APP2_MOUSE	Q06335 mus musculu
8	1155.5	28.5	650	1	APP1_HUMAN	P51693 homo sapien
9	1150.5	28.4	653	1	APP1_MOUSE	Q03157 mus musculu
10	737.5	18.2	886	1	A4_DROME	P14599 drosophila
11	457	11.3	87	1	A4_MACFA	P53601 macaca fasc
12	403	9.9	76	1	A4_MACMU	P29216 macaca mula
13	292	7.2	59	1	A4_BOVIN	Q28053 bos taurus
14	288	7.1	58	1	A4_RABIT	Q28748 oryctolagus
15	288	7.1	58	1	A4_SHEEP	Q28757 ovis aries
16	287	7.1	58	1	A4_CANFA	Q28280 canis famil
17	283	7.0	57	1	A4_PIG	Q29023 sus scrofa
18	283	7.0	57	1	A4_URSUMA	Q29149 ursus marit
19	194.5	4.8	3911	1	AKA9_HUMAN	Q99996 h a-kinase
20	186	4.6	252	1	SPT2_HUMAN	Q43291 homo sapien
21	186	4.6	993	1	SCP1_MOUSE	Q62209 mus musculu
22	176	4.3	55	1	ISH1_STOHE	P31713 stoichactis
23	175.5	4.3	579	1	G160_HUMAN	Q08378 homo sapien
24	175	4.3	302	1	TFPI_RAT	Q02445 rattus norv
25	174.5	4.3	252	1	SPT2_MOUSE	Q9WU03 mus musculu
26	174.5	4.3	513	1	SPT1_HUMAN	Q02455 homo sapien
27	169	4.2	1875	1	MLP1_YEAST	Q02455 saccharomyc
28	168	4.1	304	1	TFPI_HUMAN	P10646 homo sapien
29	166	4.1	55	1	ISH2_STOHE	P81129 stoichactis
30	164.5	4.1	507	1	SPT1_MOUSE	Q9T097 mus musculu
31	163.5	4.0	346	1	AMB_MERUN	Q62577 meriones un
32	163.5	4.0	1130	1	YL17_CAEEL	Q11102 caenorhabdi
33	163	4.0	2944	1	CA17_HUMAN	Q02388 homo sapien

34	163	4.0	3176	1	CA36_HUMAN	P12111 homo sapien
35	162	4.0	304	1	TFPI_MACMU	Q28864 macaca mula
36	162	4.0	407	1	IE68_HSVSA	Q01042 herpesvirus
37	162	4.0	3137	1	CA36_CHICK	P15989 gallus gall
38	161.5	4.0	630	1	YCF2_OENVI	P31569 oenothera v
39	161.5	4.0	1278	1	DYNA_HUMAN	Q14203 homo sapien
40	161	4.0	64	1	SPT3_HUMAN	P49223 homo sapien
41	160.5	4.0	721	1	YCF2_OENPI	P31568 oenothera p
42	160	3.9	802	1	NAB3_YEAST	P38996 saccharomyc
43	159	3.9	197	1	MCPI_MELCP	P82968 melithaea c
44	158.5	3.9	2004	1	MOZ_HUMAN	Q92794 homo sapien
45	158	3.9	58	1	ISIK_HELPO	P00994 helix pomat

ALIGNMENTS

RESULT 1	ID	A4_HUMAN	STANDARD:	PRT:	770 AA.
AC	P05067;	P09000;	Q16011;		
DT	13-AUG-1987	(Rel. 05, Created)			
DT	01-NOV-1991	(Rel. 20, last sequence update)			
DT	16-OCT-2001	(Rel. 40, last annotation update)			
DE	Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)				
DE	(PN-II) (APP) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].				
GN	APP OR A4 OR CVAP OR AD1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;				
RC	MEDLINE=87144572; PubMed=2881207;				
RX	Kang J., Lemaire H.G., Unterbeck A., Salbaum J.M., Masters C.L.,				
RA	Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;				
RT	"The precursor of Alzheimer's disease amyloid A4 protein resembles a				
RT	cell-surface receptor.";				
RL	Nature 325:733-736(1987).				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=88122639; PubMed=2893289;				
RX	Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,				
RA	Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,				
RA	Cordell B.;				
RT	"A new A4 amyloid mRNA contains a domain homologous to serine				
RT	protease inhibitors.";				
RL	Nature 331:525-527(1988).				
RN	[3]	SEQUENCE FROM N.A.			
RP	MEDLINE=89128427; PubMed=2783775;				
RX	Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,				
RA	Unterbeck A., Beyreuther K., Mueller-Hill B.;				
RT	"The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid				
RT	is encoded by 16 exons.";				
RL	Nucleic Acids Res. 17:517-522(1989).				
RN	[4]	SEQUENCE FROM N.A.			
RP	MEDLINE=97263807; PubMed=9108164;				
RX	Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,				
RA	Saito M., Tsukuni S., Sakaki Y.;				
RT	"A novel method for making nested deletions and its application for				
RT	sequencing of a 300 kb region of human APP locus.";				
RL	Nucleic Acids Res. 25:1802-1808(1997).				
RN	[5]	SEQUENCE OF 286-345 AND 365-366 FROM N.A.			
RP	MEDLINE=88122640; PubMed=2893290;				
RX	Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,				
RA	Gusella J.F., Neve R.L.;				
RT	"Protease inhibitor domain encoded by an amyloid protein precursor				
RT	mRNA associated with Alzheimer's disease.";				
RL	Nature 331:528-530(1988).				

RN [6]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [7]
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RL mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtelotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angioathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RL microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikata S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [11]
RP SEQUENCE OF 1-10 FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=89016647; PubMed=3140222;
RT Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RL encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nosttrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin II.";
RL Nature 341:144-147(1989).
RN [14]
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).";
RL Nature 362:75-79(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
RN [19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
RN [20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
RN [21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
RN [23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT water.";
RL J. Struct. Biol. 130:130-141(2000).
RN [24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=88296437; PubMed=2900137;
RA Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.6e-204;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGLNMHMNVQNGKWDSPSGTK 60
QY TCIDTKEGILQYCCQEVYPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
Db TCIDTKEGILQYCCQEVYPELQITNVEANQPTIQNMCKRGRKQCKTHPHFVIRCLVG 120
QY EFVSDALLVPDKCKFLHGERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
Db EFVSDALLVPDKCKFLHGERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
QY GVEFVCCPLAESDNVDSADAEDSDVWVGADIDYADGSEDKVEVAEEEEVAVEEEE 240
Db GVEFVCCPLAESDNVDSADAEDSDVWVGADIDYADGSEDKVEVAEEEEVAVEEEE 240
QY EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
Db EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
QY RAMISRWYFDVTEGKCAPFFYGGCGGNRNFTDEEYCAVCGSAMSQSLKTQGEPLARD 360
Db RAMISRWYFDVTEGKCAPFFYGGCGGNRNFTDEEYCAVCGSAMSQSLKTQGEPLARD 360
QY PVKLPTASTPDVADKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db PVKLPTASTPDVADKILETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
QY KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETIHMAVEMLNDRRRLALENYITAL 480
Db KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETIHMAVEMLNDRRRLALENYITAL 480
QY QAVPPRPVRHVENMLKKYVRAEQKDRQHTLKHFEHVRAVDPKKAQIRSQVMTHLRIYER 540
Db QAVPPRPVRHVENMLKKYVRAEQKDRQHTLKHFEHVRAVDPKKAQIRSQVMTHLRIYER 540
QY MNQSLILYNVPAVAEEIODEVELLQEKQNSDDVLANMISEPRISYGNDALEMSLETET 600
Db MNQSLILYNVPAVAEEIODEVELLQEKQNSDDVLANMISEPRISYGNDALEMSLETET 600
QY KTTVELLPVNGEESLDDLOPWHSGADSVRPANTENEVEPVDAARPAADRGLTTRPSGLTN 660
Db KTTVELLPVNGEESLDDLOPWHSGADSVRPANTENEVEPVDAARPAADRGLTTRPSGLTN 660
QY IKTEEISEVKMDAEFRHDSGYEVNHOKLVFFAEDVGSNKGAILGLMVGVIATVITTL 720
Db IKTEEISEVKMDAEFRHDSGYEVNHOKLVFFAEDVGSNKGAILGLMVGVIATVITTL 720
QY VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMÖN 770
Db VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMÖN 770

RESULT 2
A4_RAT STANDARD: PRT: 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein, homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RL in rat brain suggests a role in cell contact.";
RN EMO J. 7:1365-1370(1988).
[2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL: X07648; CAA30488.1; -.
DR EMBL: X14066; CAA32229.1; -.
DR PIR: S00550; S00550.
DR PIR: S03607; S03607.
DR HSSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT -----
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 759 762
FT SITE 291 341
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT CARBOHYD 571 571
FT VARSPLIC 289 289
FT VARSPLIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B2D929A7 CRC64;

Query Match 97.0%; Score 3937; DB 1; Length 770;

DR	HSSP; P05067; 1QCM.
DR	MGD; MGI:88059; App.
DR	InterPro; IPR001868; A4_APP.
DR	InterPro; IPR002223; Kunitz_BPTI.
DR	Pfam; PF02177; A4_EXTRA; 1.
DR	Pfam; PF00014; Kunitz_BPTI; 1.
DR	PRINTS; PR00203; AMYLOIDA4.
DR	PRINTS; PR00759; BASICPTASE.
DR	SMART; SM00006; A4_EXTRA; 1.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00319; A4_EXTRA; 1.
DR	PROSITE; PS00320; A4_INTRA; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW	Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW	Alternative splicing; Serine protease inhibitor.
FT	SIGNAL
FT	1
FT	17
FT	CHAIN
FT	18
FT	770
FT	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT	HOMOLOG.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).
FT	EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT	BPTI/KUNITZ INHIBITOR.
FT	CLATHRIN-BINDING (BY SIMILARITY).
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	DISULFID
FT	291
FT	341
FT	324
FT	DISULFID
FT	300
FT	316
FT	337
FT	CARBOHYD
FT	542
FT	542
FT	571
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FT	CARBOHYD
FT	571
FT	289
FT	289
FT	VARSPIC
FT	290
FT	364
FT	VARSPIC
FT	346
FT	380
FT	SEQUENCE
FT	770 AA; 86752 MW; 26C50DE0890CAFA7A CRC64;

Query Match	96.88;	Score 3927;	DB 1;	Length 770;
Best Local Similarity	96.88;	Pred. No. 1.7e-197;		
Matches 745; Conservative		7; Mismatches 18;	Indels 0;	Gaps 0

QY	1	MBGLALLLLAAWTA	RAL	LEVPTDGNAGL	AEPOIAMFCGRLNMHMNVQNGKWDSDPSG	60	
Db	1	MLPSSLALLLLAAW	T	VRAL	LEVPTDGNAGL	AEPOIAMFCGRLNMHMNVQNGKWDSDPSG	60
QY	61	TCIDTKEGILÖYCQ	ÖE	VYPELOITN	VNEANO	PVTIQNWCKRGRKÖCKTHPHFVPIRCLVG	120
Db	61	TCIGTKEGILÖYCQ	ÖE	VYPELOITN	VNEANO	PVTIQNWCKRGRKÖCKTHTHIYIPYRCLVG	120
QY	121	EFVSDALLVPDKCK	FLHÖERMDVCETHLH	MHTVAKETCSEKSTNLHDYGMLLPBGIDKFR	180		
Db	121	EFVSDALLVPDKCK	FLHÖERMDVCETHLH	MHTVAKETCSEKSTNLHDYGMLLPBGIDKFR	180		
QY	181	GVEFVCCPLAEESD	NVDSADAEEDSDV	WMGGADTDYADGSEDKV	VEVAEEEEEVAEEVEE	240	
Db	181	GVEFVCCPLAEESD	NVDSADAEEDSDV	WMGGADTDYADGSEDKV	VEVAEEEEEVAEEVEE	240	
QY	241	EADDEDEDGEDGE	VEE	EAEPYEEATERT	TSIA	TTTTTTSVEEVEVREVCSEQAE	300
Db	241	EADDEDEDGEDGE	VEE	EAEPYEEATERT	TSIA	TTTTTTSVEEVEVREVCSEQAE	300
QY	301	RAMISRWFYDVTG	KCAPFYGCGGGRNN	PDTEEYCM	AVCGSAMSÖSLKTQOEPLARD	360	
Db	301	RAMISRWFYDVTG	KCAPFYGCGGGRNN	PDTEEYCM	AVCGSAMSÖSLKTQOEPLARD	360	
QY	361	PVKLP	TTA	STPDAVDKYLE	TPGDENE	HAHFÖKAKERLEAKHRERMSQVMREWEAE	420
Db	361	PVKLP	TTA	STPDAVDKYLE	TPGDENE	HAHFÖKAKERLEAKHRERMSQVMREWEAE	420
QY	421	KNLEPKADKKAVIÖ	HÖE	KVESLEÖE	EAANERÖLVETHMAR	VEAMLNDRRLALENYITAL	480
Db	421	KNLEPKADKKAVIÖ	HÖE	KVESLEÖE	EAANERÖLVETHMAR	VEAMLNDRRLALENYITAL	480
QY	481	QAVPBRPRHVENML	KKYVRAEÖKDRÖ	HTLKHFEHVR	AVDPKKAQÖIRSQV	MHLRVIYER	540
Db	481	QAVPBRPRHVENML	KKYVRAEÖKDRÖ	HTLKHFEHVR	AVDPKKAQÖIRSQV	MHLRVIYER	540

Db	481	QAVPRPHVENVMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSQWTHLRIYER	540
QY	541	MNOSLSLLYNVPVAVAEIQDEVEDELLOKEQONSDDVLANMISEPRISYGNDALMPSLTET	600
Db	541	MNOSLSLLYNVPVAVAEIQDEVEDELLOKEQONSDDVLANMISEPRISYGNDALMPSLTET	600
QY	601	KTTVELLPVNGEFSDDLQPMHSEFGADSVPANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEFSDDLQPMHSEFGADSVPANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
QY	661	IKTEEISEVKMDAEFRHDSGEYVHHOKLVFFAEDVGSNKGAIIGLMWGVVIAIVITL	720
Db	661	IKTEEISEVKMDAEFRHDSGEYVHHOKLVFFAEDVGSNKGAIIGLMWGVVIAIVITL	720
QY	721	VMLKKQYTSIHGVEVVDAAVTPPERHLSKMQONGYENPTYKFFEQMON	770
Db	721	VMLKKQYTSIHGVEVVDAAVTPPERHLSKMQONGYENPTYKFFEQMON	770

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RESULT 4
A4_SAISC                                STANDARD:          PRT;          751 AA.
ID   A4_SAISC                                STANDARD:          PRT;          751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-
DE   amyloid protein (Beta-ApP) (A-beta)].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver, and Kidney;
RX   MEDLINE=96108492; Pubmed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC   INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC   G(O).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC   WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC   RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC   NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC   PHOSPHORYLATION (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR001868; A4_APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.

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DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 96.6%; Score 3921.5; DB 1; Length 751;
Best Local Similarity 96.9%; Pred. No. 3.2e-197;
Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMYQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMYQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYQEQVYPELOITNVVEANQPVTIQNMCKRGKCKTHPHFVIRCLVG 120
DB 61 TCIDTKEGILQYQEQVYPELOITNVVEANQPVTIQNMCKRKCKTHPHIVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLMHTVAKETCSEKSTLNHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLMHTVAKETCSEKSTLNHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSEDKYVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSEDKYVEVAEEVEAEVEE 240
QY 241 EADDEDEDEGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
DB 241 EADDEDEDEGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQAETGPC 300
QY 301 RAMISRWYFDYTEGKCAPFFYGGCGGNRNNEDTEEYCMVCGSAMQSLLKTQEP LARD 360
DB 301 RAMISRWYFDYTEGKCAPFFYGGCGGNRNNEDTEEYCMVCGSAMQSLLKTQEP LARD 360
QY 361 PVKLPFTAATPDVADVKYLETPGDENEHAFQAKERLEAKHREMSQVREWEAEARQA 420
DB 361 PVKLPFTAATPDVADVKYLETPGDENEHAFQAKERLEAKHREMSQVREWEAEARQA 420
QY 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
DB 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
DB 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIER 540
QY 541 MNQSLSLYNPVPAVAEIQDEVDDELQKEQNSDYDLANMISEPRISYGNDAIMPSTLET 600
DB 541 MNQSLSLYNPVPAVAEIQDEVDDELQKEQNSDYDLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTVLELLPVNGEFSLDLQPMHSEFADSVRPANTENEVEVPDARPADRGLTTRPGSGLTN 660
DB 601 KTVLELLPVNGEFSLDLQPMHSEFADSVRPANTENEVEVPDARPADRGLTTRPGSGLTN 660
QY 661 IKTEEISEYKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVGGVVIATVIVITL 720
DB 661 IKTEEISEYKMDAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLVGGVVIATVIVITL 720
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEQMON 770
DB 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEQMON 770

DB 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFFEQMON 751
|||||
RESULT 5
APP2_HUMAN
ID APP2_HUMAN STANDARD; PRT; 763 AA.
AC 006481;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE (CDEI-box binding protein) (CDEBP).
GN APLP2 OR APLP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8485127;
RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA Norris K., Foster D.C.;
RT "Molecular cloning of the cDNA for a human amyloid precursor protein
RT homolog: evidence for a multigene family."
RL Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT "A human amyloid precursor-like protein is highly homologous to a
RT mouse sequence-specific DNA-binding protein."
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RT "Isolation and characterization of APLP2 encoding a homologue of the
RT Alzheimer's associated amyloid beta protein precursor."
RL Nat. Genet. 5:95-99(1993).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTCAATG-3' (CDEI BOX).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, 1 (SHOWN HERE), 2 AND
CC 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC AND ENDOTHELIAL TISSUES.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
CC EMBL; S60099; AAC60589.1; -;
CC EMBL; L09209; AAA35526.1; -;
CC EMBL; Z22572; CAA80295.1; -;
CC EMBL; L27631; AAC41701.1; -;
CC HSSP; P05067; 1MWP.
CC MIM; 104776; -;
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.

DR pfam; PF02177; A4_EXTRA; 1.
DR pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Transmembrane; Signal; Alternative splicing; DNA-binding;
KW Nuclear protein; Serine protease inhibitor.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 693 716 POTENTIAL.
FT DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 215 280 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 215 231 POLY-GLU.
FT ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 310 360 BY SIMILARITY.
FT DISULFID 319 343 BY SIMILARITY.
FT DISULFID 335 356 BY SIMILARITY.
FT VARSPPLIC 308 363 MISSING (IN ISOFORM 2).
FT VARSPPLIC 613 624 MISSING (IN ISOFORM 3).
FT CONFLICT 543 543 S -> I (IN REF. 1).
SQ SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;

Query Match 48.8%; Score 1981.5; DB 1; Length 763;
Best Local Similarity 50.4%; Pred. No. 3.2e-96;
Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

QY 5 LALLLLAAMTARALEV-----PTDGNAG--LLAEPOIAMFCGRLLNMHMNVQNGKWDSDP 56
DB 15 LLLLLLVGLTAPALALAGYIEALANAGTGFVAEPQIAMFCGKLMHVNITGKWEPPD 74
QY 57 SGTKTCTIDTKEGLQYQCEVYPELOITNVANQPTIOWCKRGKCKGKTHPHFVPIYR 116
DB 75 TGTKSCFETKEEVLQYQCEMPPELOITNVMEANQRFVSIQWCRDKKQCKS--RFVTPFK 132

QY 117 CLVGEFVSDALLVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLDHYGMLPCGI 176
DB 133 CLVGEFVSDVLLVPEKQCFHKEKMEVCENHQHMTVKEACLTQGMPLYSYGMLLPCGV 192
QY 177 DKFRGVEFVCCPLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVYVAEEEEVAE 236
DB 193 DQFHGTEYVCCPQTKIIGSVSKEEEDDEE-----EEEEDEEEDYDYKSEFTEAD 245
QY 237 VEE--EEA--DDEDEDDEDEVEEEAE-----EPYEATERTSTATTITTTTESVE 284
DB 246 LEDFTEAAVDEDEDEEEGEVEVEDRDYIYDFPKDDYNE--ENPTEPGSDGTMSDKEIT 303

QY 285 EVVREVCSEQAETGRCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNEFTTEYCMACVCSA 344
DB 304 HDVKAVCSQEAAMTGCRVAVPRWYFDLSKGCVRFIYGGCGGNRNNEFSEEDYCMACVCSAM 363
QY 345 MSQSLKTQEPRLADPVKLPPTAASPDAVDKYLETPGDENEHNAHFQAKERLEAKHRE 404
DB 364 I-----PPTPLPT-----NDVDYFETSADDNEHARFQAKEQLEIRHRN 403

QY 405 RMSQVMEWEWEAEARQAKNLPKADKKAVIDQHFQEKVESLEQEAANERQQLVETHMARVEAM 464
DB 404 RMDRVKKEWEAEALQAKNLPKAERQTLIQHQAQVKALEKEAASEKQQLVETHLARVEAM 463
QY 465 LNDRRRLALENTALQAVPRPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRNVDPKKA 524
DB 464 LNDRRMALENYIALAQSDPRPRHRIQLALRRYVRAENKDRLHTIRHYQHLAVDPEKAA 523
QY 525 QIRSQVMTHLRVIERMNSQLSLLYNPVAVAEIQDEVDLQKEQNSYSDVLANMISEP 584
DB 524 QMKSQVMTHLHVIERRNQSLSLLYKVPYVAEQIEIQEIDELQEOIR-----ADM----- 572

QY 585 RISYGNDAIMDSLETETKTVELLPVNGEFSUDDLOPWHSGADSVAPANTENEVEPVADAP 644
DB 573 -----DQFTASISSETPVDR---VSSEES-EEIPPFHPF--HPFPALPENE---DTQP 616
QY 645 AADRGLTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGYEVHHQKLVFAEDVG 696
DB 617 ELYHPM--KKGSGVGEQDGGLLGAEEKYNISKNKVDENMVIDETLDV--KEMIFNAERVG 672
QY 697 S-----NKAIGLMVGVVIAIVITVLMKKQYTSIHGVEVD 739
DB 673 GLEERESVGPLREDFSLSSSALIGLVIAVAIATVIVISLVMKRQYGTISHGIVEVD 732
QY 740 AAVTPEERHLSKMQNGYENPTYKFFEQMQ 769
DB 733 PMLTPEERHLMKNQNGYENPTYKYLEQMQ 762

RESULT 6
APP2_RAT STANDARD; PRT; 765 AA.
ID APP2_RAT
AC P15943;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
GN APLP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE OF 1-627 FROM N.A.
RC STRAIN=WISTAR; TISSUE=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RL difference to human and murine homologues.";
RL Biochim. Biophys. Acta 1219:167-170(1994).
RN [2]
RP SEQUENCE OF 575-765 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90207205; PubMed=1690887;
RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT "Characterization of cDNA encoding a human sperm membrane protein
RT related to A4 amyloid protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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CC
DR EMBL; X77934; CAA54906.1; -
DR EMBL; M31322; AAA42352.1; -
DR PIR; A35981; A35981.
DR HSSP; P05067; 1AMP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.

DR MGD; MGI:88047; APlp2.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Transmembrane; DNA-binding; Signal; Nuclear protein.
FT SIGNAL 1 29
FT CHAIN 30 695
FT DOMAIN 30 624
FT TRANSMEM 625 648
FT DOMAIN 649 695
FT DOMAIN 218 294
FT DOMAIN 218 231
FT DOMAIN 256 266
FT CARBOHYD 485 485
FT CONFLICT 185 189
SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
GMLP -> MACCC (IN REF. 3).
BEST LOCAL SIMILARITY 42.0%; SCORE 1704.5; DB 1; LENGTH 695;
Matches 371; Conservative 113; Mismatches 170; Indels 137; Gaps 24;

QY 5 LALLLLAAMTARALEY-----PTDGNAG---LLAEPOIAMFCGRLNMHMNVONGKWDSDP 56
15 LLVLLLLGLTAPPAALAGYIEALANAGTGFVAVEPOIAMLCGLNMHVNITQTKWEPDP 74
QY 57 SGTCTCIDTKEGILQYQCEVPELOITNVVEANDPVITQWCKRGKCKQCTHPHFVPIYR 116
75 TGTKSCLGTKEEVLQYQCEIYPELOITNVMEANQPVNIDSWCRDRKROCKS--HIVIPFK 132
QY 117 CLVGEFVSDALLVYDCKFLHQERMDVCETHLHWTVAKETCSEKSTNLHDYGMLLPCGI 176
133 CLVGEFVSDVLLVDPNCOFFHQERMEVCEKHQRWHTLVKEACLTGTLTYSYGMLLPCGV 192
QY 177 DKFRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEEEVAE 236
193 DQFHGTEYVCCP--QTKTVDS-----DSTMSK-----EEEE--- 221
QY 237 VEEEDADDEDDEDEGEVEEEAEPEYEATERTSIATTTTTSVEEVVREVCSQAE 296
222 -EEDEDEDEEDYDLDKSEFPTADLEDFT- -AAADEEEDDEEGEEVED- - - - - 270
QY 297 TGPCRAMISRWFYDTEGKCAPEFYGGCGGNRNNDTEEYCMNAVCGSAMSQSLKTQEP 356
271 -----RDYYID-----PF-----KGDYNEENPTE-----PSSEGTI--SDKE 301
QY 357 LARDPVKLPTAASPTDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMEWEA 416
302 IVHD-VKVPPTPLPTND-VDYVLET SADNENHARFQAKAQOLEIRHRNRMDRYKKWEA 359
QY 417 ERQAKNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENY 476
360 ELQAKNLPKTERQTLIQHFQAMVKALEKEASEKQQLVETHLARVEAMLNDRRLALENY 419
QY 477 ITALQAVPPRPRAHFNMLKKYVRAEOKDRQHTLKHFEHVRMVDPKKAQIRSQVMTHLRV 536
420 LAALQSDPPRPRLRIQALRRYVRAENKDRLHTIRHYQVLAVDPEKAQMSQVMTHLRV 479
QY 537 IYERMNOSLSLYNPAVAEIODEVDELLOKEQNSDDVLAMMISEPRISYGNDAIMP 596
480 IEERRNOSTLTLYKVPYVAQEIQEIDELLOQR-----ADM-----DQFTSS 522
QY 597 LLETKTVELLPVNGEESLDDLQPMHSGADSVANTENEVEPVDARPAADRGLTTRPGS 656
523 ISENPDVAVRSSESE-EIPPFHPLHF-----PSLSENE-----GSGMAEQDG- 565
QY 657 GLTNIKTEET-SEYKMDAEFRHDSGVEVHHQKLVFAEDVGS-----N 698
Db 566 GLIGAEKVKVINSKNKMDENMVIDETLDV--KEMIFNAERVGGLLEEPSVGPLREDFSL 623
QY 699 KGAIIGLMVGGVIATVIVITLVMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYE 758

Db 624 SNALIGLLVIAVAIAIVIVISLVMLRKRQYGTISHGIVEVDPMLTPEERHLNKQNHGYE 683
QY 759 NPTYKFEEOQM 769
Db 684 NPTYKYLEOMQ 694
RESULT 8
APPL_HUMAN
ID APPL_HUMAN STANDARD; PRT; 650 AA.
AC P51693; O00113;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP).
GN APLP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088960; Pubmed=9428684;
RA Paliaga K., Peraus G., Kregler S., Duwrtwang U., Hesse L., Multhaup G.,
RA Masters C.L., Beyreuther K., Weidemann A.;
RT "Human amyloid precursor-like protein 1--cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RL Eur. J. Biochem. 250:354-363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98180887; Pubmed=9521588;
RA Lenkkeri U., Kestila M., Lamerdin J., McCreedy P., Adamson A.,
RA Olsen A., Tryggvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RL Hum. Genet. 102:192-196(1998).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. C-TERMINALLY
CC PROCESSED IN THE GOLGI COMPLEX AND IS THEN SECRETED.
CC -I- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTICULARLY
CC IN THE CEREBRAL CORTEX POSTSYNAPTIC DENSITY.
CC -I- PTM: N- AND O-GLYCOSYLATED.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; U48437; AAB96331.1; -.
DR EMBL; AD000864; AAB50173.1; -.
DR HSSP; P05067; 1MWP.
DR MIM; 104775; -.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 21
FT CHAIN 22 650
FT DOMAIN 22 580
FT TRANSMEM 581 603
FT DOMAIN 604 650
FT DOMAIN 640 643
FT DOMAIN 241 247
FT DOMAIN 264 268
FT CARBOHYD 337 337
N-LINKED (GLCNAC. . .) (POTENTIAL).
AMYLOID-LIKE PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CLATHRIN-BINDING (POTENTIAL).
POLY-GLU.
POLY-GLU.
N-LINKED (GLCNAC. . .) (POTENTIAL).

QY	298	GPCRAMISRWYEDVTEGKCAPFYEGCGGNRNNFDTEYCMAVCGSAMSOGLKTTQEP	357
Db	282	-----VMVSR-----VT-----	288
QY	358	ARDPVKLPPTASTPRDAVDKYLETPGDENEHAFQAKERLEAKHRERMSQVREWEAE	417
Db	289	---PTPRPT-----DGDVDFYFGMPGEIGEGHEGFLRAKMDLEERRMRQINEYREWAMAD	339
QY	418	ROAKNLPKADKKAVIOHFQEKVESTLEOEAANERQOLVETHMARVEAMLNDRRLALENYI	477
Db	340	SQSKNLPKADROALNEHFQSILOTFLEEQVSGERQRLVETHATRVIALINDQRRALLEGFL	399
QY	478	TALQAVPRPRRHVENMLKKKYVRAEQDRQHTLKFHEHVRMVDPKKAAQIRSQVMTHLRVI	537
Db	400	AALQGDPRQAEKRVLMALRRYLRAEQEKQRHTLRHYQHVAAVDPEKAQOQMRQVOTHLQVI	459
QY	538	YERNQSLSLLYNVPRAVAEEIQDEYDELLQKEQNYSSDVLANMISEPRISYGNDAIMP-S	596
Db	460	EERNQSLGLDDQNPHLAQELRPQIOELL-----LAEHLGPSEL-----DASVPGS	505
QY	597	LLETKTVELLPVNGEFSLDDLQPNHSGFADSVRPANTENEVEVPDARPRADRGILTTRPGS	656
Db	506	SSEDK-----GSLQP-----PESKDDPPVTLR---KGSTDQESS	536
QY	657	GLTNIKTEEISEVKMDAEFRHDSGYEVHH--QKLVEFAEDVGSNKGAITGLMVGVVIA	713
Db	537	SSGREKLTPLEQYEQKVNASAPRGFPFHSSDIQDELAPSGTGVSREALSGLLIMGAGGG	596
QY	714	TVIVITLVM-LKKOYTSIHGVEVEYDAVTPPEERHLKSMQOONGYENPTYKFFEQ	767
Db	597	SLIVSLLLLRKKKPYGTISHGVNEVDPMLTLEEQQLRELQRHGYENPTYRFFLEE	651

```

RESULT 10
A4_DROME          STANDARD;          PRT;          886 AA.
ID
AC      A4_DROME
DT      P14599;
DE      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Beta-amyloid-like protein precursor.
GN      APPL OR VND.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
NC      NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
MEDLINE=89184650; Pubmed=2494667;
RA      Rosen D.R., Martin-Morris L., Luo L., White K.;
RT      "A Drosophila gene encoding a protein resembling the human
RT      beta-amyloid protein precursor.";
RL      Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
[2]
SEQUENCE OF 1-83 FROM N.A.
RX      MEDLINE=91184006; Pubmed=2127912;
RA      Martin-Morris L.E., White K.;
RT      "The Drosophila transcript encoded by the beta-amyloid protein
RT      precursor-like gene is restricted to the nervous system.";
RL      Development 110:185-195(1990).
-1- FUNCTION: PROBABLY CORRESPONDS TO THE PROTEIN ENCODED BY THE
CC      ESSENTIAL LOCUS VND, A GENE REQUIRED FOR EMBRYONIC NERVOUS
CC      SYSTEM DEVELOPMENT.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: APPL TRANSCRIPTS ARE FOUND IN THE CENTRAL AND
CC      PERIPHERAL NERVOUS SYSTEMS. WITHIN THE NERVOUS SYSTEM TRANSCRIPTS
CC      ARE NOT OBSERVED IN NEUROBLASTS, NEWLY GENERATED NEURONS AND AT
CC      LEAST ONE CLASS OF PRESUMED GLIAL CELLS.
-1- DEVELOPMENTAL STAGE: APPL TRANSCRIPTS ARE FOUND IN POST-MITOTIC
CC      NEURONS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS IN ALL
CC      DEVELOPMENTAL STAGES.

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CC      -1 SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; J04516; AAA28874.1; -.
CC      EMBL; X55774; CAA39294.1; -.
CC      EMBL; X55775; CAA39294.1; JOINED.
CC      PIR; A32758; A32758.
CC      HSSP; P05067; IMMP.
CC      FlyBase; FBgn0000108; Appl.
CC      InterPro; IPR001868; A4_App.
CC      Pfam; PF02177; A4_EXTRA; 1.
CC      SMART; SM00006; A4_EXTRA; 1.
CC      PROSITE; PS00319; A4_EXTRA; 1.
CC      PROSITE; PS00320; A4_INTRA; 1.
CC      Signal; Transmembrane; Amyloid; Neurogenesis.
KW      SIGNAL 1 27 POTENTIAL.
FT      CHAIN 28 886 BETA-AMYLOID-LIKE PROTEIN.
FT      DOMAIN 28 810 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 811 833 POTENTIAL.
FT      DOMAIN 834 886 CYTOPLASMIC (POTENTIAL).
FT      DOMAIN 876 879 CLATHRIN-BINDING (POTENTIAL).
FT      CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      SEQUENCE 886 AA; 98261 MW; C5C1EA4194DB5A8D CRC64;

```

	Query Match	18.2%;	Score 737.5;	DB 1;	Length 886;	
	Best Local Similarity	24.7%;	Pred. No. 2.2e-31;			
	Matches 235;	Conservative 137;	Mismatches 313;	Indels 265;	Gaps 30;	
QY	7 LLLLAAMTARALEVPTDGNAGLLA-----EPQIAMFC--GRIMHMNV-QNGKWDSPSG	58				
	: :	: :	: :	:	: : :	
Db	9 LLRLSLWVLAI-----GFAOVQAASPRMEPQIAVLCEAQIYYQPYLSEEGRWVTDLISK	63				
QY	59 T---KTCTIDTEKGILQCYQEYYPELOITNINVEANQPVTIQNWCCKRG---RKQCKTHPHFV	112				
	: :	: :	: :	: :	:	:
Db	64 KTTGPTCLRDKMMDLDYCKKAYPNRDNITIVESSHYOKIGGCROGALNAKCKGSHRWI	123				
QY	113 IPIRCLVGFEVSDALLVPDKCFLHQRMDVCETHLHMHTYAKETCSEKSTNLHDYGML	172				
	: :	:	:	:	:	:
Db	124 KPFRCL-GPFQSDALLVPECCLFDHIIINASRCMPFYVRMNTGAACAQGERGMQRTFAML	182				
QY	173 PCGIDKFRGVFVCCP-----LAESDNVD--SA	199				
	:	:	:	:	:	:
Db	183 PCGISVFSGVEFVCCPKHKETDEIHVKKTDLPVMPAAQINSANDELMNDEDSNDNSYSK	242				
QY	200 DAEDDSDVWMWGADTPDYADGSEDKVEVAEEEV-----AEV	237				
	:	:	:	:	:	:
Db	243 DANEDDDL-----DEDLMGDDEEDDMVADEAATAGCSPTNTGSSGDSNSGLDINDNEY	296				
QY	238 EE-EAADDDDEDEDGEVEEAEAPYEAA-TERTTSIAITTTTTTESVEEVREVCSQA	295				
	: : : :	:	:	:	:	:
Db	297 DSGEEDNYEEDGAGSESEEAWEASWDQSGAKVVSLSKDSSSPSAPVAPAPEKAPVKS	356				
QY	296 ETGPCRAMISRWFYDTTEKCAPEFFYGGCGGNRNFTDEEYCMAYCGSAMQSLSLKTQOE	355				
	: :	:	:	:	:	:
Db	357 ESVTSTPOL-----ASAATAFVAANSNGSGT-----GAGAPPSTAOPTSD	396				
QY	356 PLARDPVKLPTTAASTPDADVKKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWE	415				
	:	:	:	:	:	:
Db	397 P-----YTFHDPHYEHQSYKVSQKRLEESHREKVTRVMKWSD	435				
QY	416 AERQAKNLPKADKKA-----VIQHFOEKVESLEQEAANEROQLVETHMARVEAMLNR	468				
	: : : :	: :	: :	:	:	

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Db 436 LEEKYQDMRLADPKAAQSFKQRMRTARFQTSVQALEEEGNAEKHQLAAMHQRYLAHINQ 493
QY 469 RRLALENYITALQAVPPRPVRHVENMLKKYVRAEQKDRQHTLKHFEH-VRMVDP---KKA 524
Db 496 KREAMTCYQALTEQPPNAHHEKCLQKLLRALHKDRALAHYRHLNLSCGPGGLEAAA 555
QY 525 QIRSQVMTHLRVIYERMNQSILSYNPAVAEEI-----QDEV----- 562
Db 556 SERPRTLERLIDIDRAVNQSMTMLKRYBELSAKIAQLMNDYILALRSKDDIPGSSLGMS 615
QY 563 -----DELLQKEQNSDDYLAN 579
Db 616 EAEAGILDKYRVEIERKVAEKEKRLAEKQKQRAEREREKLBREKRLAEKAKVDMDLKS 675
QY 580 MISE-----PRISYNDALM-----PSLTETKTVELLPVNG 611
Db 676 QVAEQQSQPTQSSTQSQAQQQQQEKSLPGKELGPDALVTAANPNLETTKS----- 726
QY 612 EFSLDDLPWHSFGADSVPAANTENEVEPYDARPAADRGLTTRPGSGLTNIKTEISEVKM 671
727 EKDLSDTE---YGEATVSTKTQVYLPVTVDDDAVQRAVEDVAAA-----VAHQEA 773
QY 672 DAEFRHDSGYEVHHQKLVF-----FAEDVGSNK--GAIIGLMVGGVIAIVITLVM 723
Db 774 EPQVOHFMTHDLGHRRESSFLRREFRAQHAAHAKEGRNVYFTLSFAGIALMAAVFGVAVA 833
QY 724 KKKQYTSIH-HGVEVDAVTP-----EERHLSKMQONGYENPTYKFFE 766
Db 834 KWRTRSPPHAQGEIEVDQNTVTHHPIVREKIVPNNQINGYENPTYKFFE 883

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RESULT 11
A4_MACFA
ID A4_MACFA STANDARD; PRT; 87 AA.
AC P53601;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN (1)
RP *SEQUENCE FROM N.A.
RS MEDLINE=91273117; PubMed=1905108;
RT Podlinsky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; M58726; AAA36828.1; -
DR HSSP; P05067; IAAP.
DR

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DR	InterPro: IPR001868; A4_APP.
DR	InterPro: IPR002223; Kunitz_BPTI.
DR	Pfam: PF00014; Kunitz_BPTI; 1.
DR	PRINTS: PR00759; BASICPTASE.
DR	SMART: SM00131; KU; 1.
DR	PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR	PROSITE: PS00320; A4_INTRA; PARTIAL.
DR	PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW	Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW	Serine protease inhibitor.
FT	NON_TER 1 1
FT	DOMAIN 4 79 BPTI/KUNITZ INHIBITOR.
FT	ACT_SITE 16 17 REACTIVE BOND.
FT	DISULFID 6 56 BY SIMILARITY.
FT	DISULFID 15 39 BY SIMILARITY.
FT	DISULFID 31 52 BY SIMILARITY.
FT	NON_TER 87 87
SQ	SEQUENCE 87 AA; 9608 MW; B67C690DE0EE7FF CRC64;
Query Match	
Best Local Similarity 11.3%; Score 457; DB 1; Length 87;	
Matches 83; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
QY	286 VVREVCSEQAETGPCRAMISRWYFDYTEGKCAPFFYGGCGGNRNNDTEEYCMAYCGSAM 345
Db	1 VVREVCSEQAETGPCRAMISRWYFDYTEGKCAPFFYGGCGGNRNNDTEEYCMAYCGSYM 60
QY	346 SOSLLKTQOEPLARDPVKLPPTTAASP 372
Db	61 SOSLRKTTREPLTRDPVKLPPTTAASP 87

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RESULT 12
A4_MACMU
ID A4_MACMU STANDARD; PRT; 76 AA.
AC P29216;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA KOO E.H., Sisodia S.S., Price D.L.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE APP FAMILY.
CC -! SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL; X15985; CAA34116.1; .
CC PIR; S06678; S06678.
CC HSSP; P05067; 1TAW.
CC

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DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 1 76 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 13 14 REACTIVE BOND.
FT DISULFID 3 53 BY SIMILARITY.
FT DISULFID 12 36 BY SIMILARITY.
FT DISULFID 28 49 BY SIMILARITY.
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 8527 MW; 492BF3069AB082A1 CRC64;

Query Match 9.9%; Score 403; DB 1; Length 76;
Best Local Similarity 94.7%; Pred. No. 2.8e-15;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 289 EVCSQAETGPCRAMISRWFVDYTEGKCAPFFYGGCGGNRNFDTEECMAVCGSAMQS 348
Db 1 EVCSQAETGPCRAMISRWFVDYTEGKCAPFFYGGCGGNRNFDTEECMAVCGSAMQS 60

QY 349 LKKTQEPPLARDPVKL 364
Db 61 LRKTRREPLTRDPVKL 76

RESULT 13
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -
CC EMBL; X56126; CAA39591.1; -
CC HSSP; P05067; IBA4.
DR

DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 7.2%; Score 292; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 ISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIVATVITLVMLK 724
Db 1 ISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVIVATVITLVMLK 59

RESULT 14
A4_RABIT STANDARD; PRT; 58 AA.
ID A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56129; CAA39594.1; -
CC HSSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 7.1%; Score 288; DB 1; Length 58;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 1.16359 Seconds
(without alignments)
902.637 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714
Perfect score: 222
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	43	1	US-08-235-400-1
2	222	100.0	43	1	US-08-437-067-1
3	222	100.0	43	1	US-08-302-808-6
4	222	100.0	43	1	US-08-079-511-1
5	222	100.0	43	1	US-08-467-607-1
6	222	100.0	43	2	US-08-404-831-1
7	222	100.0	43	2	US-08-602-264A-3
8	222	100.0	43	2	US-08-469-362-1
9	222	100.0	43	2	US-08-612-785B-1
10	222	100.0	43	2	US-08-475-579A-1
11	222	100.0	43	2	US-08-850-392-1
12	222	100.0	43	2	US-08-986-948-6
13	222	100.0	43	2	US-08-975-977-1
14	222	100.0	43	2	US-08-817-423-1
15	222	100.0	43	2	US-08-920-162A-1
16	222	100.0	43	3	US-08-461-018A-3
17	222	100.0	43	3	US-08-976-191-1
18	222	100.0	43	3	US-08-976-179-1
19	222	100.0	43	4	US-09-216-958-3
20	222	100.0	43	4	US-09-356-931-1
21	222	100.0	43	4	US-08-733-202-1
22	222	100.0	43	4	US-08-703-675C-1
23	222	100.0	43	4	US-09-390-692-1
24	222	100.0	43	4	US-08-617-267C-1
25	222	100.0	43	4	US-09-303-655-1
26	222	100.0	47	2	US-08-609-090-10
27	222	100.0	52	2	US-08-609-090-11

28	222	100.0	53	4	US-09-173-887-5	Sequence 5, Appli
29	222	100.0	59	1	US-08-484-969-3	Sequence 3, Appli
30	222	100.0	59	1	US-08-472-627-3	Sequence 3, Appli
31	222	100.0	59	1	US-08-388-463-3	Sequence 3, Appli
32	222	100.0	63	1	US-08-462-859A-4	Sequence 4, Appli
33	222	100.0	63	1	US-08-123-659A-4	Sequence 4, Appli
34	222	100.0	63	1	US-08-464-247A-4	Sequence 4, Appli
35	222	100.0	63	1	US-08-464-248A-4	Sequence 4, Appli
36	222	100.0	99	2	US-08-422-333-3	Sequence 3, Appli
37	222	100.0	99	3	US-08-339-708A-4	Sequence 4, Appli
38	222	100.0	99	3	US-08-339-708A-8	Sequence 8, Appli
39	222	100.0	100	6	5187153-10	Patent No. 5187153
40	222	100.0	100	6	5220013-10	Patent No. 5220013
41	222	100.0	100	6	5223482-10	Patent No. 5223482
42	222	100.0	103	2	US-08-404-831-2	Sequence 2, Appli
43	222	100.0	103	2	US-08-612-785B-2	Sequence 2, Appli
44	222	100.0	103	2	US-08-475-579A-2	Sequence 2, Appli
45	222	100.0	103	2	US-08-920-162A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-235-400-1
; Sequence 1, Application US/08235400
; Patent No. 5552426
; GENERAL INFORMATION:
; APPLICANT: Lunn, William H.
; APPLICANT: Monn, James A.
; APPLICANT: Zimmerman, Dennis M.
; TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,400
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-235-400-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

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RESULT 2
US-08-437-067-1
; Sequence 1, Application US/08437067
; Patent No. 5593846
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Selkoe, Dennis J.
; APPLICANT: Schlossmacher, Michael G.
; APPLICANT: Seubert, Peter A.
; APPLICANT: Vigo-Pelfrey, Carmen
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Detection
; TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,067
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,972
; FILING DATE: 26-OCT-1992
; APPLICATION NUMBER: US 07/911,647
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-6-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-437-067-1

Query Match      100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAT 43

RESULT 3
US-08-302-808-6
; Sequence 6, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhlro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-6

Query Match      100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
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Db      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 4
US-08-079-511-1
; Sequence 1, Application US/08079511
; Patent No. 5766846
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Selkoe, Dennis J.
; APPLICANT: Schlossmacher, Michael G.
; APPLICANT: Seubert, Peter A.
; APPLICANT: Vingo-Pelfrey, Carmen
; TITLE OF INVENTION: Methods and Compositions for Detection
; TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Tower, Suite 2000

```

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,511
FILING DATE: 19930617
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,972
FILING DATE: 26-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-6-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-079-511-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 5
US-08-467-607-1
Sequence 1, Application US/08467607
Patent No. 5783434
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: TATSUNO, GWEN
APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATHESPIN AND METHODS AND
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,607
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.

REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-607-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 6
US-08-404-831-1
Sequence 1, Application US/08404831
Patent No. 5817626
GENERAL INFORMATION:
APPLICANT: Mark A. Findels, Howard Benjamin, Marc B. Garnick,
APPLICANT: Malcolm L. Gelfer, Arvind Hundal, Laura Kasman,
APPLICANT: Gary Musso, Ethan R. Signer, and James Wakefield
TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "symbol"}-Amyloid Peptide Aggre
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,831
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hanley, Elizabeth A. (EAH)
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: PPI-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-404-831-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
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Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43

RESULT 7

US-08-602-264A-3

; Sequence 3, Application US/08602264A

; Patent No. 5837853

; GENERAL INFORMATION:

; APPLICANT: Akihiko TAKASHIMA et al.

; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR

; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE

; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WENDEROTH, LIND & PONACK

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; COUNTRY: D.C.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch,

; MEDIUM TYPE: 144 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,264A

; FILING DATE: February 20, 1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/204,091

; FILING DATE: March 2, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE:

; TELEFAX:

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-602-264A-3

; Query Match

; Best Local Similarity 100.0%; Score 222; DB 2; Length 43;

; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43

RESULT 8

US-08-469-362-1

; Sequence 1, Application US/08469362

; Patent No. 5849711

; GENERAL INFORMATION:

; APPLICANT: TUNG, JAY S.

; APPLICANT: SINHA, SUKANTO

; APPLICANT: MCCONLOGUE, LISA

; APPLICANT: SEMKO, CHRISTOPHER M.F.

; TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ATHENA NEUROSCIENCES

; STREET: 800 F. Gateway Blvd.

; CITY: South San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/469,362

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: DUVALL, JEAN M.

; REGISTRATION NUMBER: 32,731

; REFERENCE/DOCKET NUMBER: 002010-005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 877-0900

; TELEFAX: (415) 877-8370

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 43 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-469-362-1

; Query Match

; Best Local Similarity 100.0%; Score 222; DB 2; Length 43;

; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43

RESULT 9

US-08-612-785B-1

; Sequence 1, Application US/08612785B

; Patent No. 5854204

; GENERAL INFORMATION:

; APPLICANT: Findeis, Mark A. et al.

; TITLE OF INVENTION: Ab peptides that modulate b-Amyloid

; TITLE OF INVENTION: Aggregation

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 28 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/612,785B

; FILING DATE: Herewith

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/404,831

; FILING DATE: 14-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/475,579

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/548,998

; FILING DATE: 27-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A.

REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43

RESULT 10
US-08-475-579A-1
Sequence 1, Application US/08475579A
Patent No. 5854215

GENERAL INFORMATION:
APPLICANT: Mark A. Flindeis et al.
TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggrega
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,579A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: PPT-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-475-579A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43

Db 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43

RESULT 11
US-08-850-392-1
Sequence 1, Application US/08850392
Patent No. 5858982

GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATHEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-8370
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-850-392-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
Db 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43

RESULT 12
US-08-986-948-6
Sequence 6, Application US/08986948
Patent No. 5955317

GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON

STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-6

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 13
US-08-975-977-1
Sequence 1, Application US/08975977
Patent No. 5965614
GENERAL INFORMATION:
APPLICANT: JAMES E. AUDIA
APPLICANT: BEVERLY K. FOLMER
APPLICANT: VARGHESE JOHN
APPLICANT: LEE H. LATIMER
APPLICANT: JEFFREY S. NISSEN
APPLICANT: JON K. REEL
APPLICANT: EUGENE D. THORSETT
APPLICANT: CELIA A. WHITESITT
TITLE OF INVENTION: N-(ARYL/HETEROARYL) AMINO
TITLE OF INVENTION: ACID ESTERS, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS

TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
ADDRESSEE: Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,977
FILING DATE: Unassigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,444
FILING DATE: 22 NO. 5965614ember 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-975-977-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 14
US-08-817-423-1
Sequence 1, Application US/08817423
Patent No. 5972634
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH E.
APPLICANT: BUSH, ASHLEY I.
APPLICANT: MOIR, ROBERT D.
TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's
TITLE OF INVENTION: Disease: Assessment of A Abnormalities
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,423
FILING DATE: 4-AUG-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/11895
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4110000/REF/JUK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-817-423-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 15
US-08-920-162A-1
Sequence 1, Application US/08920162A
Patent No. 5985242
GENERAL INFORMATION:
APPLICANT: Findeis, M. et al.
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide
TITLE OF INVENTION: Aggregation Compising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,162A
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-920-162A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Search completed: October 31, 2002, 10:13:34
Job time : 2.16359 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 1.6925 Seconds
(without alignments)
2441.270 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	57	2	E60045	Alzheimer's diseas
2	222	100.0	57	2	F60045	Alzheimer's diseas
3	222	100.0	57	2	G60045	Alzheimer's diseas
4	222	100.0	57	2	D60045	Alzheimer's diseas
5	222	100.0	57	2	A60045	Alzheimer's diseas
6	222	100.0	57	2	B60045	Alzheimer's diseas
7	222	100.0	82	2	P00438	Alzheimer's diseas
8	222	100.0	695	1	A49795	Alzheimer's diseas
9	222	100.0	770	1	ORHUA4	Alzheimer's diseas
10	217	97.7	42	2	PN0512	beta-amyloid prote
11	203	91.4	695	2	A27485	Alzheimer's diseas
12	203	91.4	695	2	S00550	Alzheimer's diseas
13	203	91.4	747	2	JH0773	Alzheimer's diseas
14	133	59.9	33	2	S23094	beta-amyloid prote
15	64	28.8	755	2	A13228	tryptophan 2-mono
16	62	27.9	755	1	DAAGWT	tryptophan 2-mono
17	62	27.9	755	1	QOAGAT	tryptophan 2-mono
18	57	25.7	327	2	S11435	genome polyprotein
19	57	25.7	503	2	S73843	general amino acid
20	56.5	25.5	378	2	S61992	SlG1 protein - yea
21	55.5	25.0	297	2	G69525	formylmethanofuran
22	55.5	25.0	621	2	AF3016	Na+/H+ antiporter
23	55.5	25.0	642	2	B98268	probable sodium/hy
24	55.5	25.0	678	2	G71526	3-methyl-2-oxobuta
25	55	24.8	291	2	F95015	glycosyl transfera
26	55	24.8	317	2	H97888	glycosyl transfera
27	55	24.8	488	2	S27652	probable aldehyde
28	55	24.8	738	2	C95936	conserved hypothet
29	55	24.8	3063	2	JS0166	genome polypeptide

30	54.5	24.5	678	2	C81683	3-methyl-2-oxobuta
31	54.5	24.5	832	2	H84848	phospholipase D (i
32	54	24.3	77	2	C97027	feoA-like protein,
33	54	24.3	284	2	S04723	genome polypeptide
34	54	24.3	316	2	D97865	hypothetical prote
35	54	24.3	322	2	E71647	hypothetical prote
36	54	24.3	763	2	A13443	Na+/H+ antiporter
37	53.5	24.1	245	2	AG1461	probable phospho-b
38	53.5	24.1	245	2	AH1098	a probable phospho
39	53.5	24.1	708	2	T24727	hypothetical prote
40	53.5	24.1	971	2	D70128	conserved hypothet
41	53	23.9	256	2	G96774	hypothetical prote
42	53	23.9	390	2	C75103	na+/h+ antiporter
43	53	23.9	422	2	D72302	hypothetical prote
44	53	23.9	601	2	T02581	nodulin-like prote
45	53	23.9	1555	2	JT0959	polypeptide - pota

ALIGNMENTS

RESULT 1
E60045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein;
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 2
F60045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein;
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 3

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079

A;Accession: G60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56126

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 4

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: D60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079

A;Accession: D60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56124

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 5

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C;Accession: A60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A;Reference number: A60045; MUID:92017079

A;Accession: A60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56125

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 6

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C;Species: Ursus maritimus (polar bear)

C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A;Reference number: A60045; MUID:92017079

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 7

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C;Accession: PQ0438; C60045

R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A;Reference number: PQ0438; MUID:93075180

A;Accession: PQ0438

A;Molecule type: DNA

A;Residues: 1-82 <DAV>

A;Cross-references: GB:M83558; GB:M83657

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A;Reference number: A60045; MUID:92017079

A;Accession: C60045

A;Molecule type: mRNA

A;Residues: 12-68 <JOH>

A;Cross-references: EMBL:X56129

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 82;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db 17 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 59

RESULT 8

A49795

Alzheimer's disease amyloid beta protein precursor - crab-eating macaque

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A49795

R;Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing

Query Match 100.0%; Score 222; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 4.3e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIIGLMVGVIAT 43
Db 597 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIIGLMVGVIAT 639

RESULT 9
AHUA4

-Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
4668; A28583; A29302; A60805; JI0038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288,'V',365-770 <LEMI>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PREI>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemic
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716,'F',718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Ander
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukul, W.; Larson, E.; Heston, L.L.; Mart
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t
A:Reference number: A44017; MUID:93035397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692,'G',694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-su
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288,'V',365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascul
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987

A/Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A/Reference number: A47584; MUID:87120328
A/Accession: A47584
A/Molecule type: mRNA
A/Residues: 674-756,'S',758-770 <GOL>
A/Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A/Experimental source: brain
R/Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A/Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A/Reference number: A47585; MUID:87120329
A/Accession: A47585
A/Molecule type: mRNA
A/Residues: 674-703 <TAN1>
A/Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R/Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A/Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A/Reference number: S02638; MUID:88296437
A/Accession: S02638
A/Molecule type: mRNA
A/Residues: 672-678 <DYR>
R/Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A/Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A/Reference number: S00707; MUID:88122640
A/Accession: S00707
A/Molecule type: mRNA
A/Residues: 286-344,'I',365-366 <TAN2>
A/Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A/Experimental source: promyelocytic leukemia cell line HL60
A/Note: alternative splice form APP(751)
R/Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A/Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A/Reference number: S00925; MUID:88122639
A/Accession: S00925
A/Molecule type: mRNA
A/Residues: 1-344,'I',365-770 <PO2>
A/Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A/Note: alternative splice form APP(751)
R/Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A/Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A/Reference number: A38949; MUID:88122641
A/Accession: A38949
A/Molecule type: mRNA
A/Residues: 287-367 <KIT>
A/Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A/Experimental source: glioblastoma cell line
A/Note: alternative splice form APP(770)
R/Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A/Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A/Reference number: A30320
A/Accession: A30320
A/Molecule type: mRNA
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 284-288,'V',365-770 <VIT1>
A/Accession: B30320
A/Molecule type: mRNA
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 122-288,'V',365-770 <VIT2>
A/Accession: C30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 606-770 <VIT3>
R/Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A/Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A/Reference number: A31087; MUID:88124954
A/Accession: A31087
A/Molecule type: mRNA

A/Residues: 507-770 <ZAI>
A/Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A/Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A/Note: the cited Genbank accession number, J03594, is not in release 101.0
R/Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. NO. 4.8e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 714
RESULT 10
PN0512
beta-amyloid protein - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C/Accession: PN0512
R/Shimohgashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A/Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A/Reference number: PN0512; MUID:93290653
A/Accession: PN0512
A/Molecule type: protein
A/Residues: 1-42 <SHI>
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C/Keywords: alternative splicing; amyloid
Query Match 97.7%; Score 217; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. NO. 8.9e-22;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42
RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N/Alternate names: proteinase nexin II
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C/Accession: A27485; S19727; I49485
R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
A/Reference number: A27485; MUID:88106489
A/Accession: A27485
A/Molecule type: mRNA
A/Residues: 1-695 <YAM>
A/Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A/Experimental source: brain
R/de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
A/Reference number: S19727; MUID:92096458
A/Accession: S19727
A/Molecule type: mRNA
A/Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A/Cross-references: EMBL:X59379
R/Iizumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A/Title: Positive and negative regulatory elements for the expression of the Alzheim
A/Reference number: I49485; MUID:92209998
A/Accession: I49485
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-19 <RES>

Thu Oct 31 10:41:53 2002

us-09-785-2_copy_672_714.rpr

Page 6

	Matches	16; Conservative	6; Mismatches	9; Indels	6; Gaps	1;
QY	7	DSGEVHHQKLVFEADVGSNKGAIIGLMVGVIAT	43			
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Search completed: October 31, 2002, 10:13:08
Job time : 4.6925 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 0.95203 Seconds
(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	57	1	A4_PIG	Q29023 sus scrofa
2	222	100.0	57	1	A4_URSM	Q29149 ursus marit
3	222	100.0	58	1	A4_CANFA	Q28280 canis famil
4	222	100.0	58	1	A4_RABIT	Q28748 corytolagus
5	222	100.0	58	1	A4_SHEEP	Q28757 ovis aries
6	222	100.0	59	1	A4_BOVIN	Q28053 bos taurus
7	222	100.0	751	1	A4_SAISC	Q95241 salmirl sci
8	222	100.0	770	1	A4_HUMAN	P05067 homo sapien
9	203	91.4	770	1	A4_MOUSE	P12023 mus musculu
10	203	91.4	770	1	A4_RAT	P04029 agrobacteri
11	62	27.9	755	1	TR2M_AGRV4	P25017 agrobacteri
12	62	27.9	755	1	TR2N_AGRVI	P21294 potato viru
13	57	25.7	327	1	POLG_PVYCH	P75462 mycoplasma
14	57	25.7	503	1	Y226_MYCPN	P54867 saccharomyc
15	56.5	25.5	378	1	SLG1_YEAST	O28076 archaeoglob
16	55.5	25.0	297	1	FTR_ARCFU	P33008 pseudomonas
17	55	24.8	488	1	DHAL_PSESP	P18247 p genome po
18	55	24.8	3063	1	POLG_PVYN	P11897 potato viru
19	54	24.3	284	1	POLG_PVYVO	Q9zcat rickettsia
20	54	24.3	322	1	Y853_RICPR	P45972 caenorhabdi
21	53.5	24.1	708	1	YNZB_CAEEL	O51246 borrelia bu
22	53.5	24.1	971	1	Y228_BORBU	P25351 saccharomyc
23	52	23.4	611	1	YCR3_YEAST	O08684 cricetus
24	51.5	23.2	1036	1	PLD1_CRIGR	O53677 mycobacteri
25	51	23.0	494	1	COBQ_MYCTU	Q06481 homo sapien
26	51	23.0	763	1	APP2_HUMAN	P32592 bos taurus
27	51	23.0	769	1	ITB2_BOVIN	P44960 haemophilus
28	50	22.5	285	1	MENB_HAEIN	P33543 arabidopsis
29	50	22.5	674	1	TML1_ARATH	O15440 homo sapien
30	50	22.5	1437	1	MRP5_HUMAN	P12651 avian infec
31	49.5	22.3	1162	1	VGL2_IBVM	P30741 cullex tarsa
32	49	22.1	246	1	TPIS_CULTA	Q9z519 streptomyce
33	49	22.1	403	1	PGK_STRCO	

34	49	22.1	542	1	YM87_MYCTU	Q50678 mycobacteri
35	49	22.1	568	1	NIRS_PSEAE	P24474 pseudomonas
36	49	22.1	695	1	APP2_MOUSE	Q06335 mus musculu
37	49	22.1	701	1	YG5L_YEAST	P53326 saccharomyc
38	49	22.1	704	1	SSP2_BOMMO	P20613 bombyx mori
39	49	22.1	753	1	PPE2_HUMAN	O14830 homo sapien
40	49	22.1	757	1	PPE2_MOUSE	O35385 mus musculu
41	49	22.1	1080	1	HDC_DROME	Q9n2m8 drosophila
42	48.5	21.8	160	1	FMDR_ECOLI	P24093 escherichia
43	48.5	21.8	330	1	COAT_PEMV	P07993 pepper mot
44	48.5	21.8	393	1	GUN1_USTMA	P54424 ustilago ma
45	48.5	21.8	459	1	Y226_MYCGE	P47468 mycoplasma

ALIGNMENTS

RESULT 1

ID	A4_PIG	STANDARD:	PRT:	57 AA.
AC	Q29023;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).			
GN	APP.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=92017079; PubMed=1656157;			
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;			
RT	"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species			
RT	polymerase chain reaction analysis."			
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).			
CC	-I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO			
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN			
CC	G(O) (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X56127; CAA39592.1; -			
DR	HSSP; P05067; IBA4.			
DR	InterPro; IPR001868; A4_APP.			
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.			
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.			
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.			
FT	NON_TER 1			
FT	CHAIN 6			
FT	DOMAIN <1			
FT	TRANSMEM 34			
FT	NON_TER 57			
FT	SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;			
SO	Query Match			
	Best Local Similarity 100.0%; Score 222; DB 1; Length 57;			
	Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
OY	1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43			

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAT 48

RESULT 2

A4_URSMA

ID A4_URSMA STANDARD; PRT; 57 AA.

AC Q29149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

DE APP.

GN Ursus maritimus (Polar bear) (Thalarcos maritimus).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Brain;

RP MEDLINE=92017079; PubMed=1656157;

RT "Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL; X56128; CAA39593.1; -.

DR HSSP; P05067; 1AML.

DR InterPro; IPR001868; A4_APP.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON_TER 57 57

SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAT 43

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAT 48

RESULT 3

A4_CANFA

ID A4_CANFA STANDARD; PRT; 58 AA.

AC Q28280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

DE APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Kidney;

RC MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL; X56125; CAA39590.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON_TER 58 58

SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 2.6e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAT 43

Db 7 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVIAT 49

RESULT 4

A4_RABIT

ID A4_RABIT STANDARD; PRT; 58 AA.

AC Q28748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

DE APP.

GN Oryctolagus cuniculus (Rabbit).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN


```
CC      G(O) (BY SIMILARITY).
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
DR      EMBL; X56129; CAA39594.1; -.
DR      HSSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 34 57 POTENTIAL.
FT      DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT      NON_TER 58
SQ      SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db      6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 5
A4_SHEEP
ID      A4_SHEEP STANDARD; PRT; 58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
NC      NCB1_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Heart;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      -----
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DR      EMBL; X56130; CAA39595.1; -.
DR      HSSP; P05067; 1AML.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 34 57 POTENTIAL.
FT      DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT      NON_TER 58
SQ      SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match      100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db      6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 6
A4_BOVIN
ID      A4_BOVIN STANDARD; PRT; 59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
GN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
NC      NCB1_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56124; CAA39589.1; -.
DR      EMBL; X56126; CAA39591.1; -.
DR      HSSP; P05067; 1BA4.
DR      InterPro; IPR001868; A4_APP.
DR      PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE; PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER 1
FT      CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 35 58 POTENTIAL.
FT      DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT      DOMAIN 59
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FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6414 MW: F43469D488A2E12D CRC64;
Query Match 100.0%; Score 222; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 7 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 49
RESULT 7
A4_SAIISC STANDARD: PRT; 751 AA.
ID A4_SAIISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; S81024; AAD14347.1; -.
DR HSSP; P05067; IAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neutone; Transmembrane; Alternative splicing; Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA: 84893 MW: 6C3E431089569049 CRC64;
Query Match 100.0%; Score 222; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 695
RESULT 8
A4_HUMAN STANDARD: PRT; 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APP) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor."
RT Nature 325:733-736(1987).
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors."
RT Nature 331:525-527(1988).
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons."
RT Nucleic Acids Res. 17:517-522(1989).
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus."
RT Nucleic Acids Res. 25:1802-1808(1997).
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";

RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

RX MEDLINE=88296437; PubMed=2900137;
RA Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease.";
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 714
Query Match 100.0%; Score 222; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.7e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 714
RESULT 9
A4_MOUSE
ID A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
01-OCT-1989 (Rel. 12, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
(Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RT is closer related to its human homolog than previously reported.";
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RT protein precursor.";
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RT Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL Gene 112:189-195(1992).
RN [6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";

RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -I- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; X59379; -; NOT_ANNOTATED_CDS.
DR EMBL; M18373; AAA37139.1; -
DR EMBL; X15210; CAA33280.1; -
DR EMBL; D10603; BAA01456.1; -
DR EMBL; M24397; AAA39929.1; -
DR PIR; A27485; A27485.
DR PIR; S04855; S04855.
DR PIR; S19727; S19727.
DR HSSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT FT
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT SITE 291 341
FT DISULFID 291 324
FT DISULFID 300 324
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT CARBOHYD 289 289
FT VARSPLIC 290 364
FT VARSPLIC 346 380
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;
Query Match 91.4%; Score 203; DB 1; Length 770;
Best Local Similarity 93.0%; Pred. No. 1.1e-18;
Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 43
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIIGLMVGVIAT 714

Db 672 DAEFGHDSGFVHRHOKLVEFAEDVGSNKGAIIGLMVGVIAT 714

RESULT 10

A4_RAT STANDARD; PRT; 770 AA.

AC P08592;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor

DE (Amyloidogenic glycoprotein) (AG).

GN APP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC -----

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CC -----

DR EMBL; X07648; CAA30488.1; -

DR EMBL; X14066; CAA32229.1; -

DR PIR; S00550; S00550.

DR PIR; S03607; S03607.

DR HSSP; P05067; 1AAP.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT FT HOMOLOG.

FT FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).

FT FT TRANSMEM 700 723 POTENTIAL.

FT FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).

FT FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.

FT FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).

FT FT DISULFID 291 341 BY SIMILARITY.

FT FT DISULFID 300 324 BY SIMILARITY.

FT FT DISULFID 316 337 BY SIMILARITY.

FT FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).

FT FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).

SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 91.4%; Score 203; DB 1; Length 770;

Best Local Similarity 93.0%; Pred. No. 1,le-18;

Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHROKLVFAEDVGSNKGAIIGLMVGVIAT 43

Db 672 DAEFGHDSGFVHRHOKLVEFAEDVGSNKGAIIGLMVGVIAT 714

|||||

RESULT 11

TR2M_AGRF4

ID TR2M_AGRF4 STANDARD; PRT; 755 AA.

AC P04029;

DT 23-OCT-1986 (Rel. 02, Created)

DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Tryptophan 2-monooxygenase (EC 1.13.12.3).

GN TMS1.

OS Agrobacterium tumefaciens.

OG Plasmid pTiAch5, and Plasmid pTiA6NC.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=358;

RN [1]

RP SEQUENCE FROM N.A.

RC PLASMID=pTiAch5;

RX MEDLINE=84207942; PubMed=6327292;

RA Giesen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H., Lemmers M., van Montagu M., Schell J.;

RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid pTiAch5.";

RT EMO J. 3:835-846(1984).

RN [2]

RP SEQUENCE FROM N.A.

RC PLASMID=pTiA6NC;

RX MEDLINE=84170374; PubMed=6584906;

RA Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D., Fuller S., Flores C., Peschon J., Nester E., Gordon M.;

RT "Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti plasmid: two gene products involved in plant tumorigenesis.";

RT Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).

CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide + CO(2) + H(2)O.

CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.

CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.

CC -1- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF P-HYDROXYBENZOTATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.

CC -1- SIMILARITY: STRONG, WITH ITS A.TUMEFACIENS PLASMID PTITM4 COUNTERPART.

CC -----

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RESULT 14
Y226_MYCPN
ID Y226_MYCPN STANDARD; PRT; 503 AA.
AC P75462;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG226 homolog (F10_orf503).
GN MPN319 OR MP517.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO M.GENITALIUM MG225.
CC -----
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CC -----
CC
DR EMBL; AE000051; AAB96165.1; -
DR InterPro; IPR002293; AA_rel_permease_1.
DR InterPro; IPR002027; Amino_acid_permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 215 235 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 359 379 POTENTIAL.
FT TRANSMEM 405 425 POTENTIAL.
FT TRANSMEM 443 463 POTENTIAL.
FT TRANSMEM 468 488 POTENTIAL.
SQ SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match 25.7%; Score 57; DB 1; Length 503;
Best Local Similarity 61.1%; Pred. No. 6.1;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 24 VGSNKGATIGLMVGCVI 41
DB 131 VKDNNGALIGLVGGFVL 148

RESULT 15
SLG1_YEAST
ID SLG1_YEAST STANDARD; PRT; 378 AA.
AC P54867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SLG1 protein precursor.
GN SLG1 OR YOR008C OR UNF378.
OS Saccharomyces cerevisiae (Baker's yeast).
```

```
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
RA Peypouquet M.F., Morel C., Doignon F., Crouzet M.;
RL submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051599; PubMed=8896276;
RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
RL which correspond to previously identified genes.";
CC yeast 12:1091-1095(1996).
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CC -----
CC
DR EMBL; U39481; AAA85862.1; -
DR EMBL; U43491; AAC49488.1; -
DR EMBL; Z74916; CAA99196.1; -
DR HSSP; P05067; 1BA6.
DR SGD; S0005534; SLG1.
DR InterPro; IPR002889; WSC.
DR Pfam; PF01822; WSC; 1.
DR SMART; SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 378 SLG1 PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 378 AA; 39270 MW; EE164F2374CCCE3 CRC64;

Query Match 25.5%; Score 56.5; DB 1; Length 378;
Best Local Similarity 42.4%; Pred. No. 5.2;
Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

OY 8 SGYEVHOKLVFAEDVGSNKGATIGLMVGCV 40
DB 251 SGSKTHKK-----ANVGATVGGVGVV 274
```

Search completed: October 31, 2002, 10:12:27
Job time : 3.95203 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 2.69742 Seconds
(without alignments)
2757.743 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714
Perfect score: 222
Sequence: 1 DAERHDSGYEVHHQKLVFF.....VGSNKGAITGLMVGVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	82	4	P78438	P78438 homo sapien
2	222	100.0	82	4	Q16014	Q16014 homo sapien
3	222	100.0	82	4	Q16019	Q16019 homo sapien
4	222	100.0	82	4	Q16020	Q16020 homo sapien
5	222	100.0	534	13	O93296	O93296 gallus gall
6	222	100.0	695	6	Q95KN7	Q95KN7 macaca fasc
7	222	100.0	695	11	O60496	O60496 cavia sp. p
8	222	100.0	695	13	O9DGJ8	O9DGJ8 gallus gall
9	222	100.0	751	13	O9DGJ7	O9DGJ7 gallus gall
10	222	100.0	770	6	O9TUI0	O9TUI0 sus scrofa
11	217	97.7	569	13	Q9PVL1	Q9PVL1 gallus gall
12	212	95.5	97	4	Q13778	Q13778 homo sapien
13	203	91.4	79	11	O35463	O35463 cricetus
14	203	91.4	607	11	O99K32	O99K32 mus musculu
15	203	91.4	693	13	O98SG0	O98SG0 xenopus lae
16	203	91.4	695	11	P97487	P97487 mus musculu

17	203	91.4	747	13	Q91963	Q91963 xenopus . ap
18	200	90.1	695	13	Q98SF9	Q98SF9 xenopus lae
19	193	86.9	699	13	O57394	O57394 narke japon
20	180	81.1	780	13	O73683	O73683 tetraodon f
21	176	79.3	33	4	Q9UC33	Q9UC33 homo sapien
22	176	79.3	737	13	O93279	O93279 fugu rubrip
23	162.5	73.2	612	13	Q919E7	Q919E7 brachydanio
24	162.5	73.2	738	13	O90W28	O90W28 brachydanio
25	162	73.0	30	4	Q9UCA9	Q9UCA9 homo sapien
26	147	66.2	28	4	Q9UCD1	Q9UCD1 homo sapien
27	126	56.8	49	6	O97917	O97917 bos taurus
28	106	47.7	19	4	Q9UCC8	Q9UCC8 homo sapien
29	64	28.8	20	4	Q9UCB6	Q9UCB6 homo sapien
30	64	28.8	328	2	Q9RPS4	Q9RPS4 enterococcu
31	64	28.8	755	2	O9R694	O9R694 agrobacteri
32	64	28.8	755	2	Q9R717	O9R717 agrobacteri
33	64	28.8	755	2	O9R472	O9R472 agrobacteri
34	62	27.9	755	2	Q44388	Q44388 agrobacteri
35	61	27.5	755	2	Q9MWA1	Q9MWA1 agrobacteri
36	57.5	25.9	895	10	Q9AWB6	Q9AWB6 lycopersico
37	57	25.7	195	10	O22662	O22662 arabidopsis
38	57	25.7	332	12	Q9DQNS	Q9DQNS potato viru
39	57	25.7	365	12	Q9WG05	Q9WG05 potato viru
40	57	25.7	575	10	O81120	O81120 lotus japon
41	55.5	25.0	678	16	O84344	O84344 chlamydia t
42	55	24.8	291	16	Q97T23	Q97T23 streptococc
43	55	24.8	738	16	Q92VF1	Q92VF1 rhizobium m
44	54.5	24.5	678	16	Q9PK54	Q9PK54 chlamydia m
45	54.5	24.5	829	10	Q9XGT0	Q9XGT0 gossypium h

ALIGNMENTS

RESULT 1	
P78438	PRELIMINARY; PRT; 82 AA.
AC P78438;	
DT 01-MAY-1997 (TREMBLrel. 03, Created)	
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).	
GN APP.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=89392030; PubMed=2675837;	
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,	
RA Little S.P.;	
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows	
RT similarity to soybean trypsin inhibitor.";	
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).	
RN [2]	
RP SEQUENCE OF 19-48 FROM N.A.	
RX MEDLINE=87120329; PubMed=2949367;	
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,	
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;	
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic	
RT linkage near the Alzheimer locus.";	
RL Science 235:880-884(1987).	
RN [3]	
RP SEQUENCE OF 32-63 FROM N.A.	
RX MEDLINE=93035397; PubMed=1415269;	
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,	
RA Anderson L., O'dahl S., Nemens E., White J.A.;	
RT "Linkage and mutational analysis of familial Alzheimer disease	
RT kindreds for the APP gene region.";	
RL Am. J. Hum. Genet. 51:998-1014(1992).	
DR EMBL; M29270; AAA51768.1; -	
DR EMBL; M29269; AAA51768.1; JOINED.	

DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 17 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 59

RESULT 2

ID Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DE BETA-AMYLROID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; Pubmed=8476439;

RA Denman R.B., Rosenzwaig R., Miller D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; AAB26263.2; -.

DR HSSP; P05067; 1BA4.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 3

ID Q16019 PRELIMINARY; PRT; 82 AA.

AC Q16019; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DE BETA-AMYLROID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; Pubmed=8476439;

RA Denman R.B., Rosenzwaig R., Miller D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61380; AAB26264.2; -.

DR HSSP; P05067; 1BA4.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 4

ID Q16020 PRELIMINARY; PRT; 82 AA.

AC Q16020; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DE BETA-AMYLROID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; Pubmed=8476439;

RA Denman R.B., Rosenzwaig R., Miller D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61383; AAB26265.2; -.

DR HSSP; P05067; 1BA4.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 5

ID O93296 PRELIMINARY; PRT; 534 AA.

AC O93296; 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)

DE AMYLROID PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98337885; Pubmed=9671674;

RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,

Milligan C.E.;

RT "Increased production of amyloid precursor protein provides a

substrate for caspase-3 in dying motoneurons.";

RL J. Neurosci. 18:5869-5880(1998).

DR EMBL; AF042098; AAC25052.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR PRINTS; PR00203; AMYLROIDA4.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

FT NON TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66DAC92 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 436 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 478

RESULT 6

Q95KN7
ID Q95KN7 PRELIMINARY; PRT; 695 AA.

AC Q95KN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 7

Q60496
ID Q60496 PRELIMINARY; PRT; 695 AA.

AC Q60496;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.

DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 222; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 8

Q9DGJ8
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.

AC Q9DGJ8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RT EMBL; AF289218; AAG00593.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db 597 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 9

Q9DGJ7
ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.

AC Q9DGJ7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]

RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 43
Db 653 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 695

RESULT 10

ID O9TUI0 PRELIMINARY; PRT; 770 AA.
AC O9TUI0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.

SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 222; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 43
Db 672 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 714

RESULT 11

ID O9PVL1 PRELIMINARY; PRT; 569 AA.
AC O9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 97.7%; Score 217; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 42
Db 472 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 513

RESULT 12
ID O13778 PRELIMINARY; PRT; 97 AA.
AC O13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 95.5%; Score 212; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 43
Db 1 EFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGVIAT 41

RESULT 13
ID O35463 PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; .
DR HSSP; P05067; IBA4.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37E206CC3BF5F597 CRC64;

Query Match	91.4%;	Score 203;	DB 11;	Length 79;
Best Local Similarity	93.0%;	Pred. No. 3.4e-19;		
Matches 40; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
      |||| ||||:||||| ||||| ||||| ||||| ||||| |||||
Db      21 DAEFGHDSGEFVRHQKLVFAEDVGSNKGAIIGLMVGVVIAT 63
```

RESULT 14

ID	Q99K32	PRELIMINARY;	PRT;	607	AA.
AC	Q99K32;				
DT	01-JUN-2001	(TREMBLrel. 17,			Created)
DT	01-JUN-2001	(TREMBLrel. 17,			Last sequence update)
DT	01-DEC-2001	(TREMBLrel. 19,			Last annotation update)
DE	HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
OX	NCBI_TaxID=10090;				
RN	[1]				

RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match	91.48;	Score 203;	DB 11;	Length 607;
Best Local Similarity	93.08;	Pred. No. 3.6e-18;		
Matches 40; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGWVIAT 43
||| ||| : || | ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 DAEEFGHDSGEFEYRHKQLVEFAEDVGSNKGAIIGLMVGWVIAT 551

RESULT 15
Q98SGO PRELIMINARY; PRT; 693 AA.
ID Q98SGO

AC Q98SG0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

RN	[1]	SEQUENCE FROM N.A.	
RP		Van den Hurk W.H.;	
RA		Thesis (2001), Department of Biological Sciences,	
RL		University of Nijmegen, Nijmegen, Netherlands.	
RL		EMBL; AJ298150; CAC37193.1; -.	
DR		HSSP; P05067; 1H23.	
DR		InterPro; IPR001868; A4_APP.	
DR		Pfam; PF02177; A4_EXTRA; 1.	
DR		PRINTS; PR00203; AMYLOIDA4.	
DR		SMART; SM00006; A4_EXTRA; 1.	
DR		PROSITE; PS00319; A4_EXTRA; 1.	
DR		PROSITE; PS00320; A4_INTRA; 1.	
FT		Signal.	
FT		SIGNAL.	
SEQ	SEQUENCE	693 AA; 78568 MW; CAFLDF655CLAB653 CRC64;	POTENTIAL.

Query Match	91.4%;	Score 203;	DB 13;	Length 693;
Best Local Similarity	88.4%;	Pred. No. 4.1e-18;		
Matches 38; Conservative	4;	Mismatches 1;	Indels 0;	Gaps 0;

OY I DAEFRHDSGYEVHHOKLVFFAEDVGSNGAIIGLMWGGVIAT 43
|::||::|||||:::||::|
Db 595 DSEYRHDTAYEVEHHOKLVFFAEVGSNGAIIGLMWGGVIAT 637

Search completed: October 31, 2002, 10:14:35
Job time : 4.69742 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:50 ; Search time 3.01476 Seconds
(without alignments)
1584.263 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222
Sequence: 1 DAEFRHDSGYEVHHOKLVFF.....VGSNKGALIGLMVGVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	43	15	AAR54759	Beta amyloid pepti
2	222	100.0	43	15	AAR60367	Beta-amyloid (1-43
3	222	100.0	43	15	AAR61328	Amyloid beta-prote
4	222	100.0	43	16	AAR64165	Beta amyloid prote
5	222	100.0	43	17	AAR95673	A-beta protein (43
6	222	100.0	43	18	AAW93371	Human beta-amyloid
7	222	100.0	43	19	AAW17758	Beta-amyloid pepti
8	222	100.0	43	19	AAW71378	Beta-amyloid precu
9	222	100.0	43	19	AAW51316	Natural beta-amylo
10	222	100.0	43	19	AAW40129	Human amyloid-beta
11	222	100.0	43	20	AAW42955	Beta-amyloid precu

12	222	100.0	43	20	AAW89362	Beta-amyloid pepti
13	222	100.0	43	21	AAB27020	Beta-amyloid pepti
14	222	100.0	43	21	AAB15372	Human beta-amyloid
15	222	100.0	43	21	AAB21216	Beta-amyloid pepti
16	222	100.0	43	21	AAW88390	Beta-amyloid pepti
17	222	100.0	43	21	AAW56102	Natural beta amylo
18	222	100.0	43	22	AAW78791	Human beta amyloid
19	222	100.0	43	22	AAE12508	Beta-amyloid pepti
20	222	100.0	43	22	AAB84428	Partial sequence o
21	222	100.0	43	22	AAB98986	Beta-amyloid pepti
22	222	100.0	43	22	AAB81193	Beta-amyloid pepti
23	222	100.0	43	22	AAB91778	Amyloid beta-prote
24	222	100.0	43	22	AAB91811	Amyloid beta-prote
25	222	100.0	43	22	AAB47108	Biotinylated beta-
26	222	100.0	43	22	AAB48344	Beta-amyloid pepti
27	222	100.0	45	16	AAR64169	Variant beta amylo
28	222	100.0	47	20	AAB37523	Synthetic amyloid
29	222	100.0	48	22	AAB37523	Amyloid precursor
30	222	100.0	52	16	AAW81476	Variant beta amylo
31	222	100.0	52	20	AAW81476	Synthetic amyloid
32	222	100.0	53	15	AAR55695	Sequence of uniden
33	222	100.0	53	16	AAR64168	Variant beta amylo
34	222	100.0	54	21	AAB32126	Amyloid-beta precu
35	222	100.0	55	22	AAB11482	Human APP peptide
36	222	100.0	57	21	AAB10910	Human amyloid prec
37	222	100.0	59	17	AAW05375	Amyloid precursor
38	222	100.0	59	19	AAW70863	Beta-amyloid precu
39	222	100.0	59	22	AAB84425	Partial sequence o
40	222	100.0	60	21	AAW69701	Beta-amyloid precu
41	222	100.0	63	19	AAW44747	APP-REP 751 BAP pe
42	222	100.0	63	19	AAW42976	Beta-amyloid pepti
43	222	100.0	70	22	AAE09373	Human wild-type AP
44	222	100.0	70	22	AAE09374	Human APP695 Swedi
45	222	100.0	70	22	AAE09375	Human truncated AP

ALIGNMENTS

RESULT 1	AAW54759	standard; peptide; 43 AA.
AC	AAW54759;	
XX		
DT	30-NOV-1994	(first entry)
XX		
DE	Beta amyloid peptide.	
XX		
KW	Beta amyloid peptide; amyloid plaques; Alzheimer's disease; lesion;	
KW	brain; senility; dementia; detection; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
PN	W09410569-A.	
XX		
PD	11-MAY-1994.	
XX		
PF	01-SEP-1993;	93WO-US08264.
XX		
PR	26-OCT-1992;	92US-0965972.
XX		
PA	(SCHE/) SCHENK D B.	
PA	(SCHL/) SCHLOSSMACHER M G.	
PA	(SELK/) SELKOE D.	
XX		
PI	Schenk DB, Schlossmacher MG, Selkoe DJ, Seubert PA;	
PI	Vigo-pelfreyc;	
XX		
DR	WPI, 1994-167654/20.	
XX		
PT	Detecting soluble beta-amyloid peptide concns. e.g. for	
PT	diagnosing and assessing progression of Alzheimer's disease - by	

PT exposing cultured cells to test cpd. to determine effect of cpd.
PT on produced soluble beta-amyloid peptide
XX
PS Disclosure; Page 10; 55pp; English.
XX
CC Beta amyloid peptide is the principal chemical constituent of
CC amyloid plaques, lesions found on the brains of Alzheimer's disease
CC patients. The ability to detect beta amyloid peptide in fluid
CC samples provides a means of diagnosing Alzheimer's disease.
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 2

ID AAR60367 standard; peptide; 43 AA.

AC AAR60367;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-43).

KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
anti-beta-amyloid antibody; diagnosis.

OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94WO-JP00089.

PR 25-JAN-1993; 93JP-0010132.
PR 05-FEB-1993; 93JP-0019035.
PR 16-NOV-1993; 93JP-0286985.
PR 28-DEC-1993; 93JP-0334773.

(TAKE) TAKEDA CHEM IND LTD.

Kitada C, Odaka A, Suzuki N;

WPI; 1994-264110/32.

PT Antibodies recognising specific parts of beta-amyloid - can be
used for diagnosis of diseases implicating beta-amyloid, such as
PT Alzheimer's disease

PS Disclosure; Page 83; 116pp; Japanese.

CC Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
CC from the C-terminal portion. The antibodies are useful for assaying
CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
CC disease.

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 3

ID AAR61328 standard; Protein; 43 AA.

AC AAR61328;

DT 21-APR-1995 (first entry)

DE Amyloid beta-protein, ABP.

KW Amyloid beta-protein; ABP; Tau-protein kinase I enzyme; TPK-I;
Alzheimer's disease.

OS Synthetic.

PN EP616032-A.

PD 21-SEP-1994.

PF 01-MAR-1994; 94EP-0103057.

PR 02-MAR-1993; 93JP-0041160.
PR 22-MAR-1993; 93JP-0085143.
PR 02-AUG-1993; 93JP-0191246.

PA (TAKA/) TAKASHIMA A.
(MITU) MITSUBISHI KASEI CORP.

PI Hoshino T, Imahori K, Saito K, Sato S, Shiratsuchi A;
PI Takashima A;

DR WPI; 1994-287181/36.

PT Newly isolated tau-protein kinase I enzyme - with specificity for
tau-protein providing means for prevention and treatment of
PT Alzheimer's disease

PS Example 1; Page 22; 30pp; English.

CC Amyloid beta-protein (ABP) is the main component of senile plaques
CC in Alzheimer's disease. ABP was used to demonstrate the protective
CC properties of anti-sense TPK-I oligonucleotides (AA067461 and AA067462)
CC on hippocampus cells dosed with ABP.

SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 4

ID AAR64165 standard; peptide; 43 AA.

AC AAR64165;

DT 02-AUG-1995 (first entry)

DE Beta amyloid protein.

KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
diagnosis; amyloidosis associated disease; Alzheimer's disease;

KW Down's syndrome.

XX OS Synthetic.
XX PN WO9428412-A.
XX PD 08-DEC-1994.
XX PF 27-MAY-1994; 94WO-US05809.
XX PR 28-MAY-1993; 93US-0069010.
XX PA (MIRI-) MIRIAM HOSPITAL.
XX PI Majocha RE, Marotta CA;
XX DR WPI; 1995-023013/03.
XX PT Amyloid binding composition comprising labelled amyloid protein and carrier - useful for in vivo imaging of amyloid deposits, for diagnosing Alzheimer's disease and Down's Syndrome.
PS Claim 5; Page 42; 58pp; English.
XX CC AAR64165 shows the amino acid sequence of the beta amyloid protein. The protein binds amyloid and is useful for in vivo imaging of amyloid deposits and hence diagnosis of an amyloidosis-associated disease, such as Alzheimer's disease or Down's syndrome. AAR64165-69 show specific variants generated from this generic sequence with addition amino acids.
XX SQ Sequence 43 AA;
OY Query Match 100.0%; Score 222; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 5
AAR95673
ID AAR95673 standard; Peptide; 43 AA.
XX AC AAR95673;
XX NT 24-FEB-1997 (first entry)
XX PF A-beta protein (43 amino acid version).
XX KW A-beta protein; beta-amyloid precursor protein; APP; Alzheimer's disease; diagnosis; monitor; amyloid plaque; senile.
XX OS Homo sapiens.
XX PN WO9615452-A1.
XX PD 23-MAY-1996.
XX PF 13-NOV-1995; 95WO-US14659.
XX PR 07-APR-1995; 95US-0419008.
XX PR 14-NOV-1994; 94US-0339141.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PI Barbour R, Schenk DB, Seubert PA, Vigo-pelfrey C;
XX DR WPI; 1996-260003/26.
XX PT Diagnosis and monitoring of Alzheimer's disease - by detecting abnormally low concentration of A-beta peptide extending beyond amino acid 41 in cerebrospinal fluid
PS

XX PS Disclosure; Page 16; 57pp; English.
XX CC The "amyloid-beta peptide" or A-beta is an approx. 4.2 kD protein which, in the brains of Alzheimer's disease, Down's Syndrome, HCHWA-D and some normal aged subjects, forms the subunit of amyloid filaments comprising the senile (amyloid) plaques and the amyloid deposits in small cerebral and meningeal blood vessels. A-beta is an approx. 39-43 amino acid fragment of a large membrane-spanning glycoprotein, referred to as the beta-amyloid precursor protein (APP), encoded by a gene on the long arm of human chromosome 21. Detecting the amt. of A-beta is useful in diagnosis and monitoring of Alzheimer's disease, when taken together with other clinical symptoms. The present sequence is a 43 amino acid version of A-beta.
XX SQ Sequence 43 AA;
OY Query Match 100.0%; Score 222; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 6
AAW93371
ID AAW93371 standard; Protein; 43 AA.
XX AC AAW93371;
XX DT 28-MAY-1999 (first entry)
XX DE Human beta-amyloid polypeptide.
XX KW Cathepsin Y; human; beta-amyloid peptide; BAP; secretion; inhibitor; protease; carboxypeptidase; aliphatic C-terminal amino acid; diagnostic; glycoprotein; cerebral deposition; pathogenesis; Alzheimer's disease; detection; amyloid plaque; angiotachy; brain; Trisomy 21; amyloidosis; Down's syndrome; hereditary cerebral haemorrhage.
XX OS Homo sapiens.
XX PN WO9639194-A1.
XX PD 12-DEC-1996.
XX PF 26-APR-1996; 96WO-US06211.
XX PR 06-JUN-1995; 95US-0469362.
XX PR 06-JUN-1995; 95US-0467607.
XX PR 02-MAY-1997; 97US-0850392.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PA (ANDE/) ANDERSON J.
XX PA (CHRY/) CHRYSLER S.
XX PA (MCCO/) MCCONLOGUE L.
XX PA (SINH/) SINHA S.
XX PA (TATS/) TATSUNO G.
XX PA (TUNG/) TUNG JS.
XX PI Anderson J, Chrysler S, McConlogue L, Semko CMF;
XX PI Sinha S, Tatsuno G, Tung JS;
XX DR WPI; 1997-042872/04.
XX PT Acylamino and acyl:peptido:amino alcohol and aldehyde derivs. - inhibit beta-amyloid peptide prodn. in cells, use in Alzheimer's disease, also prepn. of cathepsin Y and nucleic acid encoding for it.
XX PS Disclosure; Page 11; 90pp; English.

This invention describes the inhibition of beta-amyloid peptide production in cells is effected by administration of an acylamino or acylpeptidamino alcohol or aldehyde derivative of formula

$$R1(X)m-y-NR-CH(R2)-(CONR10-CH(R3))n-R4$$
 where R and R10 = H or 1-6C alkyl; R or R and R2 together, and/or R10 and R3 together complete a 4-10C ring structure; R1 = (a) 1-4C alkyl substd. by 1-5 substituents. chosen from 6-10C aryl (opt. substd. by 1-3 of 1-6C alkyl, 1-6C alkoxy, 6-10C aryl, 6-10C aryloxy, OH, cyano, halo and amino), 3-8C cycloalkyl or Het, in which the substd. alkyl gp. is opt. further substd. by 1 or 2 of OH; (b) 2-4C alkenyl substd. by 1-4 substituents. as for 1-4C alkyl above; (c) 6-10C aryl (opt. substd. by 1-3 substituents. as for alkyl above), (d) fluorenyl or (e) Het; Het = 3-14C heterocyclcyl contg. 1-3 N, O or S heteroatoms; R2 and R3 = D- or L- amino acid side chains of at least 2C atoms, excluding prolyl side chain; R4 = COCH=N2, CH2OH, C=NOH or COR5; R5 = H, 1-6C alkyl (opt. contg. 1 or 2 halogen atoms), 1-6C alkoxy, NR6R7 or N(Me)OMe; R6 and R7 = H or 1-6C alkyl; X = O, NR9 or S; R9 = H, 1-6C alkyl or 6-10C aryl; Y = CO or CS; m = 0 or 1; and n = 0-2; provided that (i) when R1 = 1-naphthyl, R2 = CHMe2 (L-isomer), R3 = benzyl (L-isomer), Y = CO, m = 0 and n = 1, then R4 (sic) is not N(Me)OMe; (ii) when R1 = CHPh2, R2 = p-benzoyloxybenzyl (L-isomer), Y = CO, and m = n = 0, then R4 (sic) is not N(Me)OMe; and (iii) when R1 = PhCH=CPh, Y = CO, R2 = benzyl (L-isomer) and m = n = 0, then R4 (sic) is not N(Me)OMe. Cathepsin Y is a 31 kD carboxypeptidase with particular activity for aliphatic C-terminal amino acids. It is involved in the generation of beta-amyloid protein (BAP) from its precursor glycoprotein. Cerebral deposition of BAP plays a key role in pathogenesis of Alzheimer's disease (AD), and its detection can precede openly apparent symptoms of AD by years or more. Amyloid plaques and angiopathy are also present in the brain in those having Trisomy 21 (Down's syndrome) and hereditary cerebral haemorrhage with amyloidosis of Dutch type (HCHWA-D). The inhibitors are of use in inhibiting such plaque deposition and in treating AD. The cathepsin Y can be used, by virtue of its carboxypeptidase activity, in screening for BAP prodn. inhibitors, and, more widely, as a general C-terminal protease in a variety of chemical and biological systems. Conversely, assay of cathepsin Y in body fluid can be used diagnostically to evaluate the future risk of developing AD. The nucleic acid can be used to probe specifically for presence of cathepsin Y RNA or DNA in tissues or cloned libraries. It can also be used for expression of recombinant cathepsin Y, by transfection of a host cell.

Sequence	43	AA;
5Q		

Query Match	100.0%;	Score 222;	DB 18;	Length 43;
Best Local Similarity	100.0%;	Pred. No. 1.6e-25;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

1 DAERHDSGYEVHHOKLVFFAEDVGSNGAIIGLMWGVVIAT 43
 |||
 1 DAERHDSGYEVHHOKLVFFAEDVGSNGAIIGLMWGVVIAT 43

RESULT 7	
AA17758	
ID	AA17758 standard; peptide; 43 AA.
XX	
AC	AA17758;
XX	
DT	10-AUG-1999 (first entry)
XX	
DE	Beta-amyloid peptide.
XX	
KW	Beta-amyloid peptide; beta-amyloid precursor protein; APP;
KW	membrane spanning glycoprotein; Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
PN	WO9822493-A2.
XX	
PD	28-MAY-1998.
XX	
PF	20-NOV-1997; 97WO-US18704.
XX	

PR 22-NOV-1996; 96US-0755334.

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PA (ELIL) LILLY & CO ELI.

PI Audia JE, Folmer BK, John V, Latimer LH, Nissen JS;
PI Porter WJ, Thorsett ED, Wu J;

DR WPI; 1998-322359/28.

PT New and known aryl or hetero-aryl amino acid derivatives - useful
PT for inhibiting beta-amyloid peptide release and/or its synthesis and
PT treating Alzheimer's disease

PS Disclosure; Page 19; 131pp; English.

CC The present invention describes a composition comprising an inert carrier
CC and an N-(aryl or heteroaryl) amino acid, derivative e.g.

CC N-[N-(3,4-dichlorophenyl)alaninyl] valine methyl ester. The composition
CC can be used for inhibiting beta-amyloid peptide release and/or its
CC synthesis in a cell, for preventing the onset of Alzheimer's disease
CC and for treating Alzheimer's disease in order to inhibit further
CC deterioration. The dosage is 0.1-500 mg/kg/day orally, rectally,
CC transdermally, subcutaneously or intravenously. The present sequence
CC represents the beta-amyloid peptide.

... SQ Sequence 43 AA;

Query Match	100.0%;	Score 222;	DB 19;	Length 43;
Best Local Similarity	100.0%;	Pred. No. 1.6e-25;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 8
AAW71378

ID AAW71378 standard; peptide; 43 AA.

AC AAW71378;

DT 02-DEC-1998 (first entry)

DE Beta-amyloid precursor protein epitope.

...
KW Beta amyloid precursor protein; eukaryotic cell line;
KW exogenous gene construction; identification; quantification;
KW inhibitor; beta-amyloid processing; treatment; Alzheimer's disease;
KW brain trauma; Downs syndrome.

05 Homo sapiens.

PN W09837215-A1.

PD 27-AUG-1998.

03-FEB-1998; 98WO-US01899.

PR 31-JUL-1997; 97US-0904296.

PR	02-APR-1997;	97US-0825737.
PR	24 FEB 1997,	97US-0804371.

PA (HMRI) HOECHST MARION ROUSSEL INC.

PA (SCIO-) SCIOS INC.

PI Cordell B, Huggins J, Mischak RP, Pruss R, Rautmann G;

PI Scardina JM;

.... WPI; 1998-495368/42.
DR

PT New eukaryotic cell lines - containing a gene construct containing a

PT beta-amyloid precursor protein encoding sequence, used for
PT identifying inhibitors of beta-amyloid processing
PS Disclosure; Fig 5; 82pp; English.
XX
CC The present sequence represents an epitope derived from a beta amyloid
CC precursor protein, and recognised by antibodies BA#1, 108.1, 1702.1,
CC and 1101.1. The specification describes an eukaryotic cell line
CC having exogenous gene construction comprising a cytomegalovirus (CMV)
CC promoter, a strong ribosome binding site (RBS), a beta-amyloid
CC precursor protein (BAPP) nucleic acid sequence, a selectable marker,
CC and a poly-adenylation signal. The products can be used for identifying
CC or quantifying beta-amyloid protein and for identifying inhibitors of
CC beta-amyloid processing. They can be used to develop products for
CC treating amyloidoses, e.g. Alzheimer's disease, brain trauma or Downs
CC syndrome.
CC
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 19; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db
RESULT 9
AAW51316
ID AAW51316 standard; peptide; 43 AA.
XX
AC AAW51316;
XX
DT 14-AUG-1998 (first entry)
XX
DE Natural beta-amyloid peptide fragment.
XX
KW Natural beta-amyloid peptide; aggregation; D-amino acid;
KW Alzheimer's disease; beta-amyloidosis.
XX
OS Homo sapiens.
XX
PN WO9808868-A1.
XX
PD 05-MAR-1998.
XX
PT 27-AUG-1997; 97WO-US15166.
XX
PR 21-JUL-1997; 97US-0897342.
PR 27-AUG-1996; 96US-0703675.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Arico-muendel CC, Chin J, Findeis MA, Gefter ML;
PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
PI Musso G, Phillips K, Signer ER, Wakefield J;
XX
DR WPI; 1998-216936/19.
XX
PT Peptide compounds which are preferably based on beta-amyloid
PT peptide(s) - are useful in treatment of disorders related to
PT beta-amyloidosis, especially Alzheimer's disease
XX
PS Disclosure; Page 8; 92pp; English.
XX
CC The invention relates to peptides that modulate natural beta-amyloid
CC peptide aggregation. The modulators of the invention comprise a peptide
CC preferably based on a beta-amyloid peptide, that is comprised entirely
CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
CC residues and includes at least two D-amino acid residues independently
CC selected from the group consisting of D-leucine, D-phenylalanine and
CC D-valine. Preferred amino-terminal modifying groups include cyclic,

CC heterocyclic, polycyclic and branched alkyl groups. Preferred
CC carboxy-terminal modifying groups include an amide group, an alkyl amide
CC group, an aryl amide group or a hydroxy group. The peptides may be used
CC to treat disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease. They may also be used in methods for detecting the
CC presence of beta-amyloid peptides in biological samples. The present
CC sequence represents the 43 amino acid long form of natural beta-amyloid
CC peptide.
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 19; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
Db
RESULT 10
AAW40129
ID AAW40129 standard; peptide; 43 AA.
XX
AC AAW40129;
XX
DT 03-JUN-1998 (first entry)
XX
DE Human amyloid-beta peptide.
XX
KW Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiopathy;
KW brain; membrane-spanning glycoprotein; beta-amyloid precursor protein;
KW APP; chromosome 21; human; Alzheimer's disease; AD; amyloid filament;
KW treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.
XX
OS Homo sapiens.
XX
PN WO9748983-A1.
XX
PD 24-DEC-1997.
XX
PF 18-JUN-1997; 97WO-US10601.
XX
PR 18-JUN-1996; 96US-0665649.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Citron M, Schenk D, Selkoe DJ, Seubert PA;
XX
DR WPI; 1998-063287/06.
XX
PT Identifying compounds that alter cellular production of amyloid-beta
PT 42 fragment - in vitro or in transgenic animal models, potentially
PT useful for treatment of Alzheimer's and other amyloid deposition
PT diseases
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence represents a human amyloid-beta peptide (A-beta) which is a
CC fragment of the of a large membrane-spanning glycoprotein referred to as
CC the beta-amyloid precursor protein (APP) encoded by a gene on the long
CC arm of chromosome 21. This peptide is also known as the beta-AP peptide
CC and forms the subunit of the amyloid filaments comprising senile
CC (amyloid) plaques and the amyloid deposits in small cerebral and
CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be
CC a 39-43 amino acid fragment. This invention provides methods of screening
CC compounds for their ability to alter the production of the A-beta
CC peptide, which is composed of >41 amino acids, alone, or in combination
CC with the A-beta peptide composed of 40 amino acids or less. Such agents
CC that reduce the production of the A-beta peptide are potentially useful
CC for treatment of Alzheimer's Disease or other diseases involving amyloid
CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with

CC amyloidosis of Dutch type and advanced aging of the brain.
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 19; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 11
ID AAY42955 standard; protein; 43 AA.
XX
AC AAY42955;
02-JAN-2000 (first entry)
XX
XX Beta-amyloid precursor protein.
XX
KW Beta-amyloid precursor protein; APP; release inhibition;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN US5965614-A.
XX
PD 12-OCT-1999.
XX
PF 21-NOV-1997; 97US-0975977.
XX
PR 22-NOV-1996; 96US-0104593.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Folmer BK, Audia JE, Latimer LH, Nissen JS, Reel JK, Thorsett ED;
PI Whitesitt CA, John V;
XX
DR WPI; 1999-579933/49.
XX
XX Process for inhibiting beta-amyloid peptide cellular release and/or
PT synthesis comprising administration of N-(aryl/heteroaryl) amino acid
PT ester derivatives, useful for treatment and prevention of Alzheimer's
PT disease -
XX
XX Disclosure; Column 49; 29pp; English.
XX
CC New chemical compounds are disclosed which inhibit the cellular
CC release and/or synthesis of beta-amyloid peptide (the present sequence).
CC The compounds are N-(aryl or heteroaryl) amino acid ester derivatives, of
CC which N-(3,4-dichlorophenyl)alanine ethyl ester is a specific example.
CC These compounds can be used for the treatment and prevention of
CC Alzheimer's disease.
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 20; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 12
ID AAW89362 standard; peptide; 43 AA.
XX
XX AAW89362;
AC AAW89362;
XX

XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-1-43.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findels MA, Garnick MB, Gelfer ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
XX
DR WPI; 1999-094964/08.
XX
XX New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX
XX Example 1; Column 46; 52pp; English.
XX
XX The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.
XX
SQ Sequence 43 AA;
Query Match 100.0%; Score 222; DB 20; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
RESULT 13
ID AAB27020 standard; protein; 43 AA.
XX
XX AAB27020;
AC AAB27020;
XX
DT 02-FEB-2001 (first entry)
XX
DE Beta-amyloid peptide.
XX
KW Beta-amyloid peptide; nootropic; neuroprotective; Alzheimer's disease.
XX

QY 299 PCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMAYCGSAMQSLSLKTQOEPLA 358
Db 290 ----- 289
QY 359 RDPVKLPTTAASTPDVADKYLETPGDENEHAFQAKERLEAKHBRMSQVMREWEAEAR 418
Db 290 -----PATAVSTPDVADKYLENPNDENEHDFLKAKERLEGGHREKMSQVMREWEAEAR 343
QY 419 QAKNLPKADKKAVIDQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYIT 478
Db 344 QAKNLPKADKKAVIDQHFQEKVESLEQEAANERQQLVETHMARVEATLNDRRRLALENYIT 403
QY 479 ALQAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYI 538
Db 404 ALQADPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIN 463
QY 539 ERMNQSLLYNPVAVAEIQDEVDLQKQNSDDVLAMNISEPRISYGNDAIMPST 598
Db 464 ERMNQSLLYNPVAVAEIQDEVDLQKQNSDDVLAMNISEPRISYGNDAIMPST 523
QY 599 ETKTVELLPVNGEFSDDLQPMHSGADSPANTENEVERPVDARPAADRGLTTRPGSGL 658
Db 524 ETKTVELLPVNGEFSDDLQPMHSGADSPANTENEVERPVDARPAADRGLTTRPGSGL 583
QY 659 TNKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGATIGLVGGVVIATVIVI 718
Db 584 TNKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGATIGLVGGVVIATVIVI 643
QY 719 TLVMLKKQOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 770
Db 644 TLVMLKKQOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQOMON 695

RESULT 10

Q99K32 PRELIMINARY: PRT: 607 AA.
ID Q99K32: PRELIMINARY: PRT: 607 AA.
AC Q99K32: PRELIMINARY: PRT: 607 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE=;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -
DR HSSP; P05067; 1AAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 75.5%; Score 3065; DB 11; Length 607;
Best Local Similarity 96.9%; Pred. No. 2.9e-183;
Matches 588; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
QY 164 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDNDSDADAEEDDSDVWVGADTDYADGSED 223
|||||

Db 1 NLHDYGMLLPCGIDKFRGVEFVCCPLAEESDSDSDADAEEDDSDVWVGADTDYADGSED 60
QY 224 KVEVAEEEEVAEEEEADDEDDEDEDEVEEBAEPEPEAEATERTTSTATTTTTTESV 283
Db 61 KVEVAEEEEVAEEEEADDEDDEDEDEVEEBAEPEPEAEATERTTSTATTTTTTESV 120
QY 284 EEVREVCSEQAEETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMAYCGS 343
Db 121 EEVREVCSEQAEETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEEYCMAYCGS 180
QY 344 AMSQSLKTQOEPLARDPVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHR 403
Db 181 VSTQSLKTQOEPLARDPVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHR 240
QY 404 ERMQVREWEAEARQAKNLPKADKKAVIDQHFQEKVESLEQEAANERQQLVETHMARVEA 463
Db 241 ERMQVREWEAEARQAKNLPKADKKAVIDQHFQEKVESLEQEAANERQQLVETHMARVEA 300
QY 464 MLNDRRLALENYITLQAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 523
Db 301 MLNDRRLALENYITLQAVPPRRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKA 360
QY 524 AQIRSQVMTHLRVIERMNSLSLLYNPVAVAEIQDEVDLQKQNSDDVLAMNISE 583
Db 361 AQIRSQVMTHLRVIERMNSLSLLYNPVAVAEIQDEVDLQKQNSDDVLAMNISE 420
QY 584 PRISYGNDAIMPSTETKTVELLPVNGEFSDDLQPMHSGADSPANTENEVERPVDAR 643
Db 421 PRISYGNDAIMPSTETKTVELLPVNGEFSDDLQPMHSGADSPANTENEVERPVDAR 480
QY 644 PAADRGLTTRPGSGLTNKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGATII 703
Db 481 PAADRGLTTRPGSGLTNKTEEISEVKMDAEFRHDSGYEVHHQKLVFEADVGSNKGATII 540
QY 704 GLWVGVIATVIVITLMLKKQOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYK 763
Db 541 GLWVGVIATVIVITLMLKKQOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYK 600
QY 764 FFEQOMON 770
Db 601 FFEQOMON 607

RESULT 11

O57394 PRELIMINARY: PRT: 699 AA.
ID O57394: PRELIMINARY: PRT: 699 AA.
AC O57394: PRELIMINARY: PRT: 699 AA.
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EL AMYLOID PRECURSOR PROTEIN 699.
GN EL App699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristigaster; Batoida;
OC Torpediniformes; Narcinoidae; Narkidae; Narke.
OX NCBI_TaxID=62965;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=ELECTRIC LOBE;
RX MEDLINE=98129705; Pubmed=9461486;
RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA Suzuki T.;
RT "cDNA isolation of Alzheimer's amyloid precursor protein from
RT cholinergic nerve terminals of the electric organ of the electric
RT ray."
RL Biochem. J. 330:29-33(1998).
DR EMBL; AB005544; BAA24230.1; -
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.

Db 421 KNLPRADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENTITAL 480

OY 481 QAVPPRRHVFMMLKKYVRAEOKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYI 537

Db 481 QAVPPRRHVFMMLKKYVRAEOKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLMPYI 537

RESULT 13

O90W28 PRELIMINARY; PRT; 738 AA.

AC O90W28: 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE AMYLOID PRECURSOR PROTEIN.

GN APP.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

NCBI_TaxID=7955;

SEQUENCE FROM N.A.

RA Groth C., Lardelli M.;

RT "Expression analysis of zebrafish app.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF389401; AAK64495.1; -

SQ SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

Query Match 68.6%; Score 2785.5; DB 13; Length 738;

Best local Similarity 69.9%; Pred. No. 1e-165;

Matches 540; Conservative 85; Mismatches 101; Indels 47; Gaps 14;

OY 5 LALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNHMNVQNGKWDSPSGTKCID 64

Db 6 LFILMAVASTLAVEVPSDGTGLLAEPQIAMFCGKLNMTINIQSGKWEPPDPSGSKSIG 65

OY 65 TREGLIQCOEVPPELOITNVYANOPVTIONWCKRGRKCKTHPHFVIRCLVGEFVS 124

Db 66 NKEGILQYCOEVPPELOITNVYANOPVSIWDMCKSKRCKRSHMHIIVPYRCLVGEFVS 125

OY 125 DALIVPDKCKFLHOERMDVCEHLHMTVAKETCSEKSTNHDYGMLLPCGIDKFRGYEF 184

Db 126 DALIVPDKCKFLHOERMDVCEHLHMTVAKESCGRSMNHDYGMLLPCGIDRFRGYEF 185

OY 185 VCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEEVEEAD 244

Db 186 VCCP-ADAGKESESAAVEEDSDVWVGAEADYTENSMT-DAAPAVLE-DDEDADE 241

OY 245 DED-DEGD----EVEEAEDEEATERTT-SIATTTTTTESVEEVREVCSQAET 297

Db 242 EEDDQDGDGRDEKIEEEEEE-EERTOSTSALTSTTTTESVEEVREVCFASAE 299

OY 298 GPCRAMISRWFYDTEGKCAPFEYGGCGGNRNNDTEEYCAVCGSAMSQSLKTQEP 357

Db 300 GPCRAMLSRWYVREERCAPIYIGCGGNRNNEFESEYCLSVCSGV----- 346

OY 358 ARDPVKLPTTAASPDAVDKYLETPGDENEHAHFOKAKERLEAKHREMSQVMREWEAE 417

Db 347 -----LPTSSSPDAVDRIETPADENEHAHFLKAKESLETKHREMSQVMREWEAE 400

OY 418 RQAKNLPRADKKAVIQHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENTI 477

Db 401 RQAKSLPRNDKKAVIQHFQEKVEALEQESASERQOLVETHMARVEALLNDRRLALESYL 460

OY 478 TALQAVPPRRHVFMMLKKYVRAEOKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYI 537

Db 461 SALQADPPRRHVFSILKKYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRPQVLTHLRYI 520

OY 538 YERNMOSLSLLYNPAVAEIQDEVDLLQKEQNSDDVLANMISEPRISYGDALMPSL 597

Db 521 EERNMOSLGLLKYVPGVADDIODOV-ELLQREQQEMSAQLANQSDARVSYGDALMPDS 579

OY 598 TETKTVELLPVNGEFSLLDLOPMHSFGADSVPAANTEVEVPVDARPADRGLTTRPGSG 657

Db 580 T---AGLELLPAEDTQGEFIHP-ESFN---QPNTHNOVEPVDARPPDLDLATRPVSG 631

OY 658 LTNKTEISEVKMDAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMWGVVIAVYI 717

Db 632 L---KPDDIPELRMEAEERHS---EVYHOKLVFAEDVSSNKGAIIGLMWGVVIAVYI 685

OY 718 ITLVMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGENPTYKFEQOMON 770

Db 686 ITLVMLRKQYTSIHGILEVDAVTPPEERHLSKMQONGENPTYKFEQOMHN 738

RESULT 14

O73683 PRELIMINARY; PRT; 780 AA.

AC O73683: 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].

GN APP.

OS Tetraodon fluviatilis (Puffer fish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

NCBI_TaxID=47145;

SEQUENCE FROM N.A.

RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;

RT "Analysis of pufferfish homologues of the At-rich human APP gene.";

RL Gene 210:17-24(1998).

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.

DR EMBL; AF018165; AAC41275.1; -

DR HSSP; P05067; 1H23.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Serine protease inhibitor.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT CHAIN 19 780 HOMOLOG.

FT CHAIN 682 724 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN 19 711 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 712 732 POTENTIAL.

FT DOMAIN 733 780 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 323 382 BPTI/KUNITZ INHIBITOR.

FT SITE 769 772 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 327 378 BY SIMILARITY.

FT DISULFID 336 361 BY SIMILARITY.
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 68.1%; Score 2763.5; DB 13; Length 780;
Best Local Similarity 67.4%; Pred. No. 2.6e-164;
Matches 541; Conservative 80; Mismatches 113; Indels 69; Gaps 11;

OY 7 LLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVONGKWDSPSGTKTCIDTK 66
Db 8 LLLVAAASTLAEVPTDVSMLGLAEPOVAMFCGKINMHINVOGKWEPPDSGKSCIGTK 67
OY 67 EGILOYCQEVYPELOITNVANQPVITQNMCKRGKQCKTHPHFVTPYRCLVGEFVSDA 126
Db 68 EGILOYCQEVYPELOITNVANQPVISQNMCKRGKQCRSHMHIVPYRCLVGEFVSDA 127
OY 127 LTVPDCKCKFLHOERMDVCEHLMHTVAKETCESEKSTNLHDYGMLLPCGIDKRGVEFYC 186
Db 128 LTVPDCKCKFLHOERMNOCESHLMHTVAKESCGDRAMNLHDYGMLLPCGIDRFRGVEFYC 187
OY 187 CPLAEESDNVDSADAEDSDVWVGADTDYADGS-----EDKVEVAEEEE 232
Db 188 CP-AEAERDMSTEKDADDSDVWVGADNDYSDNSMVRPEPEAEQOEETRPSVVEEEEG 246
OY 233 EVAVEVEEE-----ADDEDEDEDEGEVEEEAEPEYEATERSTISA 273
Db 247 EVAOEDDEEEVLDTDQDGDGEDHEAADDEEEEDVDEIDAFGESDDVDADDEPTNVA 306
OY 274 ----TTTTTTSVEEVVREVCSGEAETGPCRAMISRWFYDVEGKA-PFFYGGCGGNRN 329
Db 307 MTTTTTTTTTTSVEEVVRMFCMAHADTGPTASMPSWYFDVADGRTMYELMYGGCGGNMN 366
OY 330 NEDTEEYCMVCGSAMSQSLKTTQEPRLARDPVKLPPTAASDPDAVDKYLETPGDENENHA 389
Db 367 NFESEYCLSVCSV-----VPTDMPSSPDADVHYLETPADENENHA 407
OY 390 HFOKAKERLEAKHRERMSQVREWEAEARQAKNLPKADKAVIQHFOEKVESLEQEAANE 449
Db 408 HFOKAKESLEAKHRERMSQVREWEAEARQAKNLPKADKAVIQHFOEKVEALEQEAASE 467
OY 450 RQOLVETHMARVEAMLNDRRLALENYITALQAVPRPRHVENMLKKYVRAEQKDRQHTL 509
Db 468 RQOLVETHMARVEALLNDRRLALENYITALQODPRPRHVSFLKKYVRAEQKDRQHTL 527
OY 510 KHEHVRMVDPKKAAQIRSQVMTLRLVIYERMNQSLLYNVPAVAEEIODEVDELQKE 569
Db 528 KHEHVRMVDPKKAAQIRPOYLTLRLVIEERMNQSLLYKVPVADDIQDOV-ELLQRE 586
OY 570 QNYSDDVLANMISEPRISYGDALMPSLTETKTTVELLPVNGEFSLDDLQPMH--SEGAD 627
Db 587 QAEMAQOLANLOTDVRSYGDALMPDQELGDAQADLPR--QEDTLGGVGFVHPSEFN-- 642
OY 628 SVPANTENEVEVPDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHDSGYEVHOK 687
Db 643 --QNTENOVEPVDSPRPFERGVPTRP--VTGKSMEAVPELMEETEDRQSTEEYEVHOK 697
OY 688 LVFEAEDVGSNKGAIIIGLMVGVVIAVIVITLVMLKKKQYTSIHGVEVEVDAVTPPEER 747
Db 698 LVFEAEDVGSNKGAIIIGLMVGVVIAVIVITLVMLRKQYTSIHGIIIEVDAVTPPEER 757
OY 748 HLSKMQONGYENPTYKFFEQMON 770
Db 758 HLSKMQONGYENPTYKFFEQMON 780

RESULT 15
O9PVL1 PRELIMINARY: PRT; 569 AA.
AC O9PVL1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).

GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 67.0%; Score 2717; DB 13; Length 569;
Best Local Similarity 82.5%; Pred. No. 1.4e-161;
Matches 534; Conservative 15; Mismatches 18; Indels 80; Gaps 5;

OY 126 ALLVPDKCKFLHOERMDVCEHLMHTVAKETCESEKSTNLHDYGMLLPCGIDKRGVEFY 185
Db 1 ALLVPDKCKFLHOERMDVCEHLMHTVAKESCEKSMNLHDYGMLLSCGIDKRGVEFY 60
OY 186 CPLAEESDNVDSADAEDSDVWVGADTDYADGSSEDKVE--VAEEVEVAEEBEAD 243
Db 61 CPLAEESDNLDSADAEDSDVWVGADADYADGSDDKVEEQPEDELLFVVEDEDAD 120
OY 244 DDEDEDEGEVEEEAEPEYEATERSTSIATTTTTTTSVEEVVREVCSGEAETGPCRAM 303
Db 121 DD-DDDDGET-EETEEYEATERSTSIATTTTTTTSVEEVVR----- 163
OY 304 ISRWFYDTEGKCAPFFYGGCGGNRNFDTEEYCMVCGSAMSQSLKTTQEPRLARDPVK 363
Db 164 ----- 163
OY 364 LPTTAASPDVADKYLETPGDENENAHFOKAKERLEAKHRERMSQVREWEAEARQAKNL 423
Db 164 VPTTAASPDVVDKYLETPGDENENAHFOKAKERLEAKHRERMSQVREWEAEARQAKNL 223
OY 424 PKADKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAV 483
Db 224 PKADKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQTV 283
OY 484 PRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNO 543
Db 284 PRPRHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNO 343
OY 544 SLSLLYNVPAVAEEIODEVDELQKEQNSDDVLANMISEPRISYGDALMPSLTETKTT 603
Db 344 SLSFLYNVPAVAEEIODEVDELQKEQNSDDVLANMISEPRISYGDALMPSLTETKTT 403
OY 604 VELLPVNGEFSLDDLQPMHSGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNIKT 663
Db 404 VELLPVNGEFSLDDLQPMHSGVDSVPANTENEVEVPDARPAADRGLTTRPGSGLTNVKT 463
OY 664 EEISEVKMDAEFRHDSGYEVHOKLVFEAEDVGSNKGAIIIGLMVGVVIAVIVITLVML 723
Db 464 EEVSEVKMDAEFRHDSGYEVHOKLVFEAEDVGSNKGAIIIGLMVGVVIANVIVITLVML 523
OY 724 KKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
Db 524 KKKQYTSIHGVEVDAVTP-ERHLSKMQONGYENPTYKFFEQMON 569

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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 17.048 Seconds
(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLPGLALLLAAMTARALEV.....KMQNGYENPTYKFEQMON 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	4058	100.0	770	1 A4_HUMAN	P05067 homo sapien
2	3937	97.0	770	1 A4_RAT	P08592 rattus norv
3	3927	96.8	770	1 A4_MOUSE	P12023 mus musculu
4	3921.5	96.6	751	1 A4_SAIISC	Q05241 salmtril sci
5	1981.5	48.8	763	1 APP2_HUMAN	Q06481 homo sapien
6	1971.5	48.6	765	1 APP2_MOUSE	P15943 rattus norv
7	1704.5	42.0	695	1 APP2_MOUSE	Q06335 mus musculu
8	1155.5	28.5	650	1 APP1_HUMAN	P51693 homo sapien
9	1150.5	28.4	653	1 APP1_MOUSE	Q03157 mus musculu
10	737.5	18.2	886	1 A4_DROME	P14599 drosophila
11	457	11.3	87	1 A4_MACFA	P53601 macaca fasc
12	403	9.9	76	1 A4_MACMU	P29216 macaca mula
13	292	7.2	59	1 A4_BOVIN	Q28053 bos taurus
14	288	7.1	58	1 A4_RABIT	Q28748 coryctolagus
15	288	7.1	58	1 A4_SHEEP	Q28757 ovis aries
16	287	7.1	58	1 A4_CANFA	Q28280 canis famill
17	283	7.0	57	1 A4_PIG	Q29023 sus scrofa
18	283	7.0	57	1 A4_URUMA	Q29149 ursus marit
19	194.5	4.8	3911	1 AKAG_HUMAN	Q09996 h a-kinase
20	186	4.6	252	1 SPT2_HUMAN	Q43291 homo sapien
21	186	4.6	993	1 SCPI_MOUSE	Q62209 mus musculu
22	176	4.3	55	1 ISH1_STOHE	P31713 stoichiactis
23	175.5	4.3	579	1 G160_HUMAN	Q08378 homo sapien
24	175	4.3	302	1 TPPI_RAT	Q02445 rattus norv
25	174.5	4.3	252	1 SPT2_MOUSE	Q9wu03 mus musculu
26	174.5	4.3	513	1 SPT1_HUMAN	Q43278 homo sapien
27	169	4.2	1875	1 MLP1_YEAST	Q02455 saccharomyc
28	168	4.1	304	1 TPPI_HUMAN	P10646 homo sapien
29	166	4.1	55	1 ISH2_STOHE	P81129 stoichiactis
30	164.5	4.1	507	1 SPT1_MOUSE	Q09097 mus musculu
31	163.5	4.0	346	1 AMBP_MERUN	Q62577 meriones un
32	163.5	4.0	1130	1 YLI7_CAEEL	Q11102 caenorhabdt
33	163	4.0	2944	1 CA17_HUMAN	Q02388 homo sapien

34	163	4.0	3176	1 CA36_HUMAN	P12111 homo sapien
35	162	4.0	304	1 TPPI_MACMU	Q28864 macaca mula
36	162	4.0	407	1 IE68_HSVSA	O01042 herpesvirus
37	162	4.0	3137	1 CA36_CHICK	P15989 gallus galli
38	161.5	4.0	630	1 YCF2_OENVI	P31569 oenothera v
39	161.5	4.0	1278	1 DYNA_HUMAN	Q14203 homo sapien
40	161	4.0	64	1 SPT3_HUMAN	P49223 homo sapien
41	160.5	4.0	721	1 YCF2_OENPI	P31568 oenothera p
42	160	3.9	802	1 NAB3_YEAST	P38996 saccharomyc
43	159	3.9	197	1 MCP1_MEICP	P82968 melithaea c
44	158.5	3.9	2004	1 MOZ_HUMAN	Q92794 homo sapien
45	158	3.9	58	1 ISIK_HELPO	P00994 helix pomat

ALIGNMENTS

RESULT 1	ID	STANDARD;	PRT;	770 AA.
A4_HUMAN	AC	P05067; P09000; Q16011;		
A4_HUMAN	DT	13-AUG-1987 (Rel. 05, Created)		
A4_HUMAN	DT	01-NOV-1991 (Rel. 20, Last sequence update)		
A4_HUMAN	DT	16-OCT-2001 (Rel. 40, Last annotation update)		
A4_HUMAN	DE	Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)		
A4_HUMAN	DE	(PN-II) (APP) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].		
A4_HUMAN	GN	APP OR A4 OR CVAP OR ADL.		
A4_HUMAN	OS	Homo sapiens (Human).		
A4_HUMAN	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
A4_HUMAN	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
A4_HUMAN	OX	NCBI_TaxID=9606;		
A4_HUMAN	RN	[1]		
A4_HUMAN	RP	SEQUENCE FROM N.A.		
A4_HUMAN	RC	TISSUE=Brain;		
A4_HUMAN	RX	MEDLINE=87144572; PubMed=2881207;		
A4_HUMAN	RA	Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,		
A4_HUMAN	RA	Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;		
A4_HUMAN	RT	"The precursor of Alzheimer's disease amyloid A4 protein resembles a		
A4_HUMAN	RL	cell-surface receptor.";		
A4_HUMAN	RL	Nature 325:733-736(1987).		
A4_HUMAN	RN	[2]		
A4_HUMAN	RP	SEQUENCE FROM N.A.		
A4_HUMAN	RX	MEDLINE=88122639; PubMed=2893289;		
A4_HUMAN	RA	Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,		
A4_HUMAN	RA	Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,		
A4_HUMAN	RA	Cordell B.;		
A4_HUMAN	RT	"A new A4 amyloid mRNA contains a domain homologous to serine		
A4_HUMAN	RT	protease inhibitors.";		
A4_HUMAN	RL	Nature 331:525-527(1988).		
A4_HUMAN	RN	[3]		
A4_HUMAN	RP	SEQUENCE FROM N.A.		
A4_HUMAN	RX	MEDLINE=89128427; PubMed=2783775;		
A4_HUMAN	RA	Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,		
A4_HUMAN	RA	Unterbeck A., Beyreuther K., Mueller-Hill B.;		
A4_HUMAN	RT	"The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid		
A4_HUMAN	RT	is encoded by 16 exons.";		
A4_HUMAN	RL	Nucleic Acids Res. 17:517-522(1989).		
A4_HUMAN	RN	[4]		
A4_HUMAN	RP	SEQUENCE FROM N.A.		
A4_HUMAN	RX	MEDLINE=97263807; PubMed=9108164;		
A4_HUMAN	RA	Hattori M., Tsukahara F., Furihata Y., Tanahashi H., Hirose M.,		
A4_HUMAN	RA	Saito M., Tsukuni S., Sakaki Y.;		
A4_HUMAN	RT	"A novel method for making nested deletions and its application for		
A4_HUMAN	RT	sequencing of a 300 kb region of human APP locus.";		
A4_HUMAN	RL	Nucleic Acids Res. 25:1802-1808(1997).		
A4_HUMAN	RN	[5]		
A4_HUMAN	RP	SEQUENCE OF 286-345 AND 365-366 FROM N.A.		
A4_HUMAN	RX	MEDLINE=88122640; PubMed=2893290;		
A4_HUMAN	RA	Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,		
A4_HUMAN	RA	Gusella J.F., Neve R.L.;		
A4_HUMAN	RT	"Protease inhibitor domain encoded by an amyloid protein precursor		
A4_HUMAN	RT	mRNA associated with Alzheimer's disease.";		
A4_HUMAN	RL	Nature 331:528-530(1988).		

RN [6]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RL protease inhibitory activity."; Nature 331:530-532(1988).
RN [7]
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RL cerebrovascular and the neuritic plaque amyloid peptides."; Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RL Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RL disease brain: coding and noncoding regions of the fetal precursor
RN mRNA are expressed in the cortex."; Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RL Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiotensin II of Alzheimer's disease: amino acid composition
RN and partial sequence of a 4,200-dalton peptide isolated from cortical
RL microvessels."; J. Neurochem. 49:1394-1401(1987).
RN [10]
RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RL gene."; Gene 87:257-263(1990).
RN [11]
RP SEQUENCE OF 1-10 FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=89016647; PubMed=3140222;
RL Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RN encodes a 95-kDa polypeptide."; Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RL "Purification of protease nexin II from human fibroblasts."; J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RL Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RT Sinha S.;
RN "The secreted form of the Alzheimer's amyloid precursor protein with
RP the Kunitz domain is protease nexin-II."; Nature 341:144-147(1989).
RN [14]
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RL disease amyloid protein precursor."; Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,

RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RL protein G(O)."; Nature 362:75-79(1993).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
RL Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RT Parker M.W.;
RN "Crystal structure of the N-terminal, growth factor-like domain of
RP Alzheimer amyloid precursor protein."; Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
RL "X-ray crystal structure of the protease inhibitor domain of
RN Alzheimer's amyloid beta-protein precursor."; Biochemistry 29:10018-10022(1990).
RN [18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
RL Kamarcik M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RT Tamburini P.P.;
RN "Sequential NMR resonance assignment and structure determination of
RP the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RX precursor protein."; Biochemistry 30:10467-10478(1991).
RN [19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talatous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
RL "Solution structure of residues 1-28 of the amyloid beta-peptide."; Biochemistry 33:7788-7796(1994).
RN [20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RL "Three-dimensional structures of the amyloid beta peptide (25-35) in
RN membrane-mimicking environment."; Biochemistry 35:16094-16104(1996).
RN [21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RL "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RN environment. Is the membrane-spanning domain where we think it is?"; Biochemistry 37:11064-11077(1998).
RN [22]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RL "Solution structures in aqueous SDS micelles of two amyloid beta
RN peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RP site."; J. Struct. Biol. 130:142-152(2000).
RN [23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
RL Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
RN "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RP water."; J. Struct. Biol. 130:130-141(2000).
RN [24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=88296437; PubMed=2900137;
RA Dykes T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RL Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RN amyloid A4 precursor of Alzheimer's disease.";

Query Match 100.0%; Score 4058; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.6e-204;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNGKWDSPSGTK 60
QY 61 TCIDTKEGIIQYQCEVYPELOITNVNEANQVPTIQNWCKRGKQCKTHPHFVIRCLVG 120
Db 61 TCIDTKEGIIQYQCEVYPELOITNVNEANQVPTIQNWCKRGKQCKTHPHFVIRCLVG 120
QY 121 EFVSDALVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVYEVAAEEVEAEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVYEVAAEEVEAEVEE 240
QY 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQOAEITGPC 300
Db 241 EADDEDEDGDEVEEEAEPEYEATERTSIATTTTTSVEEVREVCSQOAEITGPC 300
QY 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNNDTEBYCMAVCGSAMSOSLKTQOPLARD 360
Db 301 RAMISRWYFDVTEGKCAPFEYGGCGGNRNNDTEBYCMAVCGSAMSOSLKTQOPLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHQAKERLEAKHREMSQVREWEAEERQA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHQAKERLEAKHREMSQVREWEAEERQA 420
QY 421 KNLPRADKAVIQHFOEKVESLEQEAANRQQLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRADKAVIQHFOEKVESLEQEAANRQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSOVMTHLRVIER 540
Db 481 QAVPPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAQIRSOVMTHLRVIER 540
QY 541 MNOSLSLYNVPVAVEEIQDEVDELLOEQONYSDVLANMISEPRISYGDALMPSLTET 600
Db 541 MNOSLSLYNVPVAVEEIQDEVDELLOEQONYSDVLANMISEPRISYGDALMPSLTET 600
QY 601 KTTVELLPVNGEFSLDLQPMWHSFGADSVPAANTENEVEVPDARPAADRGTLTPRGSGLTN 660
Db 601 KTTVELLPVNGEFSLDLQPMWHSFGADSVPAANTENEVEVPDARPAADRGTLTPRGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGCVIATVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGCVIATVITL 720
QY 721 VMLKKQYTSIHGVVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 770
Db 721 VMLKKQYTSIHGVVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 770

RESULT 2
A4_RAT STANDARD; PRT: 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=88312583; Pubmed=2900758;
RA Shivers B.D., Hilbich C., Multaup G., Salbaum J.M., Beyreuther K.,
RA Söberg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=89183625; Pubmed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07648; CAA30488.1; -.
CC EMBL; X14066; CAA32229.1; -.
CC PIR; S00550; S00550.
CC PIR; S03607; S03607.
CC HSSP; P05067; 1AAP.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00006; A4_EXTRA; 1.
CC SMART; SM00131; KU; 1.
CC DR PROSITE; PS00319; A4_EXTRA; 1.
CC DR PROSITE; PS00320; A4_INTRA; 1.
CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
CC Alternative splicing; Serine protease inhibitor.
CC SIGNAL 1 17
CC CHAIN 18 770
CC FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
CC FT HOMOLOG.
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM POTENTIAL.
CC FT DOMAIN 700 723
CC FT DOMAIN 724 770
CC FT DOMAIN 715 715
CC FT DOMAIN 287 345
CC FT SITE 759 762
CC FT DISULFID 291 341
CC FT DISULFID 300 324
CC FT DISULFID 316 337
CC FT CARBOHYD 542 542
CC FT CARBOHYD 571 571
CC FT VARSPLIC 289 289
CC FT VARSPLIC 290 364
CC SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 97.0%; Score 3937; DB 1; Length 770;

Best Local Similarity 96.9%; Pred. No. 5.2e-198;
Matches 746; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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QY 1 MLPLGLALLLAATARALEVPTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
Db 1 MLPSLALLLLAATVRALEVPDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTREGILOCYQOEVPPELQITNVVEANOPVTIQNMCKRGKQCKTHPHFVIRYCLVG 120
Db 61 TCIGTREGILOCYQOEVPPELQITNVVEANOPVTIQNMCKRGKQCKTHPHFVIRYCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHOERMDVCEHLMHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFYCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVAEVEE 240
Db 181 GVEFYCCPLAEESDSIDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEEAEEVAEVEE 240
QY 241 EADDEDEDDEDEVEEEAEPEYEATEERTTSIATTTTTSVEEVVREVCSEQAETGPC 300
Db 241 EADEDEDVEDGEVEEEAEPEYEATEERTTSIATTTTTSVEEVVREVCSEQAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPERYGCGGNRNNEDEEYCMVCGSAMQSOLKTTQEPRIARD 360
Db 301 RAMISRWYFDVTEGKCAPERYGCGGNRNNEDEEYCMVCGSAMQSOLKTTSEPLPD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVREWEAEARQA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVREWEAEARQA 420
QY 421 KNLPRKADKKAVIQHFOEKVESLEJOEAEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
Db 421 KNLPRKADKKAVIQHFOEKVESLEJOEAEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAQIRSOVMTHLRYIER 540
Db 481 QAVPRPRHVENMLKKYVRAEQKDRQHTLKFHEHVRMVDPKKAQIRSOVMTHLRYIER 540
QY 541 MNGSLSLLYNVPAVAEIEQDEVELLQEKQNSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNGSLSLLYNVPAVAEIEQDEVELLQEKQNSDDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTTVELLPVNGEFLDLDLPWHSFGADSVAPANTENEVEPYDARPAADRGLTTRPGSGLTN 660
Db 601 KTTVELLPVNGEFLDLDLPWHSFGADSVAPANTENEVEPYDARPAADRGLTTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHNOKLVEFAEDVGSNKGAIIGLMVGVIATVITVL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHNOKLVEFAEDVGSNKGAIIGLMVGVIATVITVL 720
QY 721 VMLKKKQYTSIHGVEVEVDAVTPPEERHLSKMOQNGYENPTYKFEQOMON 770
Db 721 VMLKKKQYTSIHGVEVEVDAVTPPEERHLSKMOQNGYENPTYKFEQOMON 770

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RESULT 3
A4_MOUSE STANDARD; PRT; 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;

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RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RL is closer related to its human homolog than previously reported.";
RN Biochim. Biophys. Acta 1129:141-143(1991).
[2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL protein precursor.";
RN Biochem. Biophys. Res. Commun. 149:665-671(1987).
[3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL precursor of Mus domesticus.";
RN Nucleic Acids Res. 17:5396-5396(1989).
[5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RN Gene 112:189-195(1992).
[6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RL for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RN Biochem. Biophys. Res. Commun. 158:906-912(1989).
RL
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC -----
CC EMBL; X59379; -; NOT ANNOTATED_CDS.
CC EMBL; M18373; AAA37139.1; -;
CC EMBL; X15210; CAA33280.1; -;
CC EMBL; D10603; BAA01456.1; -;
CC EMBL; M24397; AAA39929.1; -;
CC PIR; A27485; A27485.
CC PIR; S04855; S04855.
CC PIR; S19727; S19727.

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DR HSSP; P05067; 1QCM.
DR MGD; MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Glycoprotein: Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
HOMOLOG.
DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
TRANSMEM 700 723 POTENTIAL.
DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.
DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
DISULFID 291 341 BY SIMILARITY.
DISULFID 300 324 BY SIMILARITY.
DISULFID 316 337 BY SIMILARITY.
CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
VARSPPLIC 289 364 E -> V (IN ISOFORM APP(695)).
VARSPPLIC 290 364 MISSING (IN ISOFORM APP(695)).
VARSPPLIC 346 380 MISSING (IN ISOFORM APP(751)).
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

Query Match 96.8%; Score 3927; DB 1; Length 770;
Best Local Similarity 96.8%; Pred. No. 1.7e-197;
Matches 745; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLPGALLLLAATARALEVPTDGNAGLLAEPOIAMFCGRNMNMVNQNGKWDSPSGTK 60
DB 1 MLPSLALLLLAAMTVRALEVPDGNAGLLAEPOIAMFCGRNMNMVNQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVYPELOITNVVEANOPVTIONMCKRGRKOCKTHPHVYPRCLVG 120
DB 61 TCIGTKEGILQYCOEVYPELOITNVVEANOPVTIONMCKRGRKOCKTHPHVYPRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCEHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEAEEVAEVEE 240
DB 181 GVEFVCCPLAEESDSVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEAEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEEPEEATERETSIATTTTTTSSVEEVVREVCSQAETGPC 300
DB 241 EADDDDEDDGDEVEEAEEPEEATERETSIATTTTTTSSVEEVVREVCSQAETGPC 300
QY 301 RAMISRWFYDTEGKCAFFYGGCGGNRNNDTEEYCMAYCGSAMQSLSLKTQEPRLARD 360
DB 301 RAMISRWFYDTEGKCVPFYGGCGGNRNNDTEEYCMAYCGSVSTQSLKTTSEPLPD 360
QY 361 PVKLPFTAATPDVADKYLETPGDENEHAHFOKAKERLEAKHREMSQVMREWEAEROA 420
DB 361 PVKLPFTAATPDVADKYLETPGDENEHAHFOKAKERLEAKHREMSQVMREWEAEROA 420
QY 421 KNLPRKADKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRKADKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRVNDPKKAQIRSQVMTHLRYIER 540
DB 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRVNDPKKAQIRSQVMTHLRYIER 540

DB 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRVNDPKKAQIRSQVMTHLRYIER 540
QY 541 MNOSLLLYNVPAAVEEIODEVDELLQKEQNSDVLANMISEPRISYGNDAIMPSTLET 600
DB 541 MNOSLLLYNVPAAVEEIODEVDELLQKEQNSDVLANMISEPRISYGNDAIMPSTLET 600
QY 601 KTVLELLPVNGEFSLDDIQPMHSGADSVPAANTENEYEPVDARPADRGLTRPGSGLTN 660
DB 601 KTVLELLPVNGEFSLDDIQPMHSGADSVPAANTENEYEPVDARPADRGLTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVVIATVIYITL 720
DB 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVVIATVIYITL 720
QY 721 VMLKKQYTSIHGVEYDAVTPPEERHLKMQQNGYENPTYKFFEQMON 770
DB 721 VMLKKQYTSIHGVEYDAVTPPEERHLKMQQNGYENPTYKFFEQMON 770

RESULT 4
A4_SAISC STANDARD; PRT; 751 AA.
ID A4_SAISC
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; S81024; AAD14347.1; -.
DR HSSP; P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match

Best Local Similarity 96.6%; Score 3921.5; DB 1; Length 751;
Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

OY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHMNVONGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHMNVONGKWDSPSGTK 60
OY 61 TCIDTKEGILQYCEVYPELQITNVNEANOPVTIQNMCKRGRKCKTHPHFVIRCLVIG 120
Db 61 TCIDTKEGILQYCEVYPELQITNVNEANOPVTIQNMCKRGRKCKTHPHFVIRCLVIG 120
OY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
OY 181 GVEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVAEEEAEEVAEVEE 240
Db 181 GVEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVEVAEEEAEEVAEVEE 240
OY 241 EADDEDEDEGDEVEEAEEPEATEERTTSIATTTTTSVEEVREVCSQAETGPC 300
Db 241 EADDEDEDEGDEVEEAEEPEATEERTTSIATTTTTSVEEVREVCSQAETGPC 300
OY 301 RAMISRWYFDVTEGKCAPFYCGCGGRNNFDEEYCMAYCGSAMSQSLKTQEPILARD 360
Db 301 RAMISRWYFDVTEGKCAPFYCGCGGRNNFDEEYCMAYCGSAMSQSLKTQEPILARD 360
OY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
OY 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMAREAMLNDRRRLALENYITAL 480
Db 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMAREAMLNDRRRLALENYITAL 480
OY 462 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRYIER 540
Db 462 QAVPPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRYIER 540
OY 541 MNQSLSLYNVPAVAEEIODEVDELLQEQNYSDDVLANMISEPRISYGNDAIMPSTLET 600
Db 541 MNQSLSLYNVPAVAEEIODEVDELLQEQNYSDDVLANMISEPRISYGNDAIMPSTLET 600
OY 522 MNQSLSLYNVPAVAEEIODEVDELLQEQNYSDDVLANMISEPRISYGNDAIMPSTLET 581
Db 522 MNQSLSLYNVPAVAEEIODEVDELLQEQNYSDDVLANMISEPRISYGNDAIMPSTLET 581
OY 601 KTVLELLPVNGEFLDLDLPWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
Db 582 KTVLELLPVNGEFLDLDLPWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 641
OY 661 IKTEEISEVKMDAEFRHDSGIEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAIVITL 720
Db 642 IKTEEISEVKMDAEFRHDSGIEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAIVITL 701
OY 721 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFPEOMON 770

Db 702 VMLKKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFPEOMON 751

RESULT 5
APP2_HUMAN
ID APP2_HUMAN STANDARD; PRT; 763 AA.
AC Q06481;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE (CDEI-box binding protein) (CDEBP).
GN APLP2 OR APLP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8485127;
RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA Norris K., Foster D.C.;
RT "Molecular cloning of the cDNA for a human amyloid precursor protein
RT homolog: evidence for a multigene family.";
RL Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hanes J., Klaudiny J., Scheit K.H.;
RT "A human amyloid precursor-like protein is highly homologous to a
RT mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RT "Isolation and characterization of APLP2 encoding a homologue of the
RT Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
CC -I- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTCACATG-3' (CDEI BOX).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -I- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE), 2 AND
CC 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC AND ENDOTHELIAL TISSUES.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
CC EMBL: S60099; AAC60589.1; -;
CC EMBL: L09209; AAA35526.1; -;
CC EMBL: 222572; CAA80295.1; -;
CC EMBL: L27631; AAC41701.1; -;
CC HSSP: P05067; 1MWP.
CC MIM: 104776; -;
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_Bpti; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 DR Transmembrane; Signal; Alternative splicing; DNA-binding;
 KW Nuclear protein; Serine protease inhibitor.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 693 716 POTENTIAL.
 FT DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 215 280 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 215 231 POLY-GLU.
 FT ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 310 360 BY SIMILARITY.
 FT DISULFID 319 343 BY SIMILARITY.
 FT DISULFID 335 356 BY SIMILARITY.
 FT VARSPPLIC 308 363 MISSING (IN ISOFORM 2).
 FT VARSPPLIC 613 624 MISSING (IN ISOFORM 3).
 FT CONFLICT 543 543 S -> I (IN REF. 1).
 SQ SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;

Query Match 48.8%; Score 1981.5; DB 1; Length 763;
 Best Local Similarity 50.4%; Pred. No. 3.2e-96;
 Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

QY 5 LALLLLAAMTARALEV-----PTDGNAG---LLAEQIAMFCGRLLMHMNVQNGKWDSDP 56
 Db 15 LLLLLLGLTAPALALAGYIEALANAGTGFAVAEPQIAMFCGLMHVNIQTGKWEPPD 74
 QY 57 SGRTICIDTKEGILQYQCEVYPELQITNVEANQPTIQNCKRGKQCKTHPHFVIPIYR 116
 Db 75 TGTSCFETKEEVLQYQCEMYPELQITNVEANQRVSIDMCRDRDKQCKS--RFVTPEK 132
 QY 117 CLVGEFVSADLLVPDKCKFLHQERMDVCETHLHMTVAKETSEKSTNLHDYGMLLPGI 176
 Db 133 CLVGEFVSADLLVPDKCKFLHQERMDVCETHLHMTVAKETSEKSTNLHDYGMLLPGI 192
 QY 177 DKFRGVEFVCCPLAEESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVAEEEEVAE 236
 b 193 DQFHGTVEYCCPQTKIIGSVSKKEEEDDEE-----EEEDDEEDDYDYKSEFPTEAD 245
 QY 237 VEE--EEA--DDEDEDGDEVEEAE-----EPYEATERSTSIATTTTTEESVE 284
 Db 246 LEDFTEAAVDEDEDEDEEVEEVEDRDYYDTFGDDYNE--ENPTPEGSDGTMSDKET 303
 QY 285 EVVREYVCEQAEETGPCRAMISRMYFDVTEGKCAPFFYGGCGGNRNFDTEYCMAYCGSA 344
 Db 304 HDVKAVCSQEAAMTGPCRAVMPRWTFDLKSGKCVRFYGGCGGNRNFESEDYCMAYCKAM 363
 QY 345 MSQSLKTQTEPLARDPVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHRE 404
 Db 364 I-----PPTPLPT-----NDVDVYFETSADDNHARFQAKAQLEIRHRN 403
 QY 405 RMSQVMEWEAEERQAKNLPKADKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAM 464
 Db 404 RMDRVKKEWEAEALQAKNLPKAEQRLIQHFOAMVKALEKEASEKQQLVETHLARVEAM 463
 QY 465 LNDRRRLALENYITALQAVPPRPRAHVENMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAA 524
 Db 464 LNDRRRLALENYITALQSDPRPHRLIQALRYVRAENKDRCLHTRHQHVLAVDPEKAA 523
 QY 525 QIRSQVMTHLRVYIERMNSLSLVNPAVAEEIQDEVEDELQKEQNYSDVLAMMISEP 584
 Db 524 QMKSQVMTHLRVYIERMNSLSLVNPAVAEEIQDEVEDELQKEQNYSDVLAMMISEP 572

QY 585 RISYGNDAIMPSTETKTVTVELLPVNGEFSLLDLPWHSFGADSVAPANTENEVEVPDAP 644
 Db 573 -----DQFTASISETPDVDR---VSSEES-EEIPPFHPR--HPFPALPENE---DTQP 616
 QY 645 AADRGILTTRPGSGLTN-----IKTEE---ISEVKMDAEFRHDSGCEVHHOKLVFAEDVG 696
 Db 617 ELYHPM--KKSGVGGEQDGLGAEEKVINSKNKVDENNVIDETLDV--KEMIFNAERVG 672
 QY 697 S-----NKGAIIGLVGCVIATVIVITLVMLKKQYTSIHGVVEVD 739
 Db 673 GLEERESVGPLREDFSLSSSALIGLLVIAVAIATVIVISLVMLKKRQYGTISHGIVEVD 732
 QY 740 AAVTPEERHLSKMOQNGYENPTYKFEQOMQ 769
 Db 733 PMLTPEERHLNKMÖNHGYENPTYKYLEQOMQ 762

RESULT 6
 APP2_RAT
 ID APP2_RAT STANDARD; PRT; 765 AA.
 AC P15943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-II).
 GN APLP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-627 FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Brain, and Heart;
 RX MEDLINE=94368849; PubMed=8086458;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
 RT protein precursor-like protein 2 (APLP2/APRN): two amino acids length
 RT difference to human and murine homologues.";
 RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Mao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 CC EMBL; X77934; CAA54906.1; -
 CC EMBL; M31322; AAA42352.1; -
 CC PIR; A35981; A35981.
 CC HSSP; P05067; 1MMP.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC PRINTS; PR00759; BASICPTASE.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Alternative splicing; Serine protease inhibitor;
 KW Signal; Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
 FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 696 718 POTENTIAL.
 FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).
 FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 322 323 REACTIVE BOND (BY SIMILARITY).
 FT DISULFID 312 362 BY SIMILARITY.
 FT DISULFID 321 345 BY SIMILARITY.
 FT DISULFID 337 358 BY SIMILARITY.
 FT DOMAIN 218 229 POLY-GLU.
 FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
 FT VARSPLIC 311 365 MISSING (IN ISOFORM C AND ISOFORM D).
 FT VARSPLIC 616 627 MISSING (IN ISOFORM B AND ISOFORM D).
 FT CONFLICT 575 577 DOF -> EFV (IN REF. 2).
 SQ SEQUENCE 765 AA; 86882 MW; CF51PCCCE305A0CF CRC64;

Query Match 48.6%; Score 1971.5; DB 1; Length 765;
 Best Local Similarity 49.7%; Pred. No. 1.1e-95;
 Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

QY 5 LALLLLAAMTARALEV-----PTDGNAG--LLAEPOIAMFCGRLLMNMNVQNGKWDSDP 56
 15 LVLVLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMFCGKLMNHVNIQTGWEDP 74
 QY 57 SGTCTCIDTKEGIIQYCOEVNPEIQTNVVEANQPTIQNMCKRGKCKOCTHPFVLPYV 116
 75 TGFKSCIGTKEEVLYQCOEIYPELQITNMEANQPNIDSWCRDKKQCRS--HIVIPK 132
 QY 117 CLVGEFVSDDLVPDKCKFLHQRMDVCETHLMHTVAKETCSEKSTNLHDYGMLLPCGI 176
 133 CLVGEFVSDDLVPENCQFHFQERMEVCEKHQRWHTVKEACLTGEMTLYSTGMLLPCGV 192
 QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEDSDVWVGADITYA-DGSEDKVEVAEEEE 233
 193 DQFHGTREYVCCPQTKVVDSDSTMSKEEEEEEE--DEEDYALDKSEFTEADLEDFT 248
 QY 234 VAEVEEEADDEDEDGDEVEEEAEPEYEE-----ATERTSIATTTTTSVEEVV 287
 249 EAAADEDEDEEEEEEEGEEVEEDRDYYDSFKGDDYNEENPEPSSDGTISDKAIAHV 308
 QY 288 REVCSQAEFTGPCRAMISRWFYDTEGKCAFEYGGCGGNRNFDTEEYCMVCGSAMSQ 347
 309 KAVCSQAEAMTGPCRAVMPRWYFDLSKGCVRFIYGGCGGNRNFESEDYCMVCKTMI-- 366
 QY 348 SLKTTQEPPLARDPVKLPSTAASPTDAVDKYLETPGDENEHAHFQAKERLEAKHRERMS 407
 367 -----PPTPLPT-----NDVDVYFETSAADNEHARFQAKAQOLEIRHRSRMD 408
 QY 408 QVMREWEAEARQAKNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLND 467
 409 RVKKEWEAEALQAKNLPKAEKQTLQHFQAMVKALEKEAASEKQQLVETHLARVEAMLND 468
 QY 468 RRRLALENITLQAVPPRRPRHVNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIR 527
 469 RRRIALENYLALQSDPRPRHRIQALRRYVRAENKDRLTIRHYQHLAVDPKAAQMK 528
 QY 528 SQVMTHLVYIERMNSLSLYNPAVAEEIQDEVDDELQEQNYSDVLAMMISEPRIS 587
 529 SQVMTHLVYIEERNOSLSLYKVPYVAQEIQEIDELQEQR-----ADM----- 574
 QY 588 YGNDAIMPSTETKTVELLPVNGEFLDDLQPMHSFGADSVANTENEVEVPDARPAD 647
 575 ---DQFTSSISENPVDVR---VSSEES-EIIRPFHF--HFRPSLSENE---DTQPELY 621
 QY 648 RGLTTRPGSGLTN-----IKTEE-----ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGS-- 697

Db 622 HPM--KKGSGMAEQDGLIGAEKEVYNSKNKMDENMVIDETLDV--KEMIFNAERVGGL 677
 QY 698 -----NKAITGLMVGGVIAIVITVITVLMKKQYTSIHGVVEVDAV 742
 Db 678 EEPDSVGPLREDFSLSSSALIGLVIAVAIATVIVISLVMLKRRQYGTISHGIVEVHPML 737
 QY 743 TPERHLKMQQNGYENPTYKFFEQMO 769
 Db 738 TPERHLNKMQNHGYENPTYKYLEQMO 764
 RESULT 7
 APP2_MOUSE
 ID APP2_MOUSE STANDARD; PRT; 695 AA.
 AC O06335;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
 GN APLP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RA von der Kammer H.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-246 FROM N.A.
 RX MEDLINE=94032480; PubMed=8218408;
 RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
 RT "The complete cDNA coding sequence for the mouse CDEI binding
 protein.";
 RL Biochim. Biophys. Acta 1216:154-156(1993).
 RN [3]
 RP SEQUENCE OF 185-695 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Heart;
 RX MEDLINE=93129193; PubMed=1482349;
 RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
 RT "A murine sequence-specific DNA binding protein shows extensive local
 similarities to the amyloid precursor protein.";
 RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
 RN [4]
 RP SEQUENCE OF 1-35 FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96029629; PubMed=7592716;
 RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
 RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
 RT "The mouse APLP2 gene. Chromosomal localization and promoter
 characterization.";
 RL J. Biol. Chem. 270:25475-25480(1995).
 CC -i- FUNCTION: BINDS TO THE DNA 5'-GTCACATG-3'(CDEI BOX) WHICH PLAYS
 AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
 CC -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
 (POTENTIAL).
 CC -i- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: 222592; CAA80306.1; -
 DR EMBL: M97216; AAA20039.1; -
 DR EMBL: U34291; AAC52318.1; -
 DR PIR: JC1404; JC1404.
 DR HSSP: P05067; 1MP.

DR MGD: MGI:88047; APlp2.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR Transmembrane; DNA-binding; Signal; Nuclear protein.
KW SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 625 648 POTENTIAL.
FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 218 231 POLY-GLU.
FT DOMAIN 256 266 POLY-GLU.
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 185 189 GMLP -> MACCC (IN REF. 3).
FT SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 42.0%; Score 1704.5; DB 1; Length 695;
Best Local Similarity 46.98; Pred. No. 7.5e-82;
Matches 371; Conservative 113; Mismatches 170; Indels 137; Gaps 24;

QY 5 LALLLLAATAALEV-----PTDGNAG---LLAEPOIAMFCGRLLMHMNVQNGKWDSDP 56
DB 15 LVLVLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAMLCGKLMHVNITQTKWEPDP 74
QY 57 SGRTKCIDTKEGILOVCOEVPYELQITNVANOPVTIONCKRGKQCKTHPHFVPIYR 116
DB 75 TGTKSCLTGKEVLQYCOEITYPELOITNVMEANOPVNIDSWCRDRKROCKS-HIVIPFK 132
QY 117 CLVGEFVSDDLVPDKCKFLHOERMDVCEHLLHMTVAKETCSEKSTNLHDYGMLPCGI 176
DB 133 CLVGEFVSDDLVPDNCQFHFQERMEVCEKHQRWHTLVKEACITGELTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAEESDNDVSADAEEDSDVWVGADFDYADGSEDKVEVAEEVEYAE 236
DB 193 DQFHGTGVCCP--QTKTVDS-----DSTMSK-----EEEE--- 221
QY 237 VEEEDADDEDEDGDEVEEEAEEDYEATERTSIATTTTTTSEVEEVVREVCSEQAE 296
DB 222 -EEDEDEEDDYDLKSEFTEADLEDFTE--AAADEEEDEEEGEVEED----- 270
QY 297 TGPCRAMISRWYFDVTEGKCAPFFYGGCCGGRNRPDTEEYCAVCGSAMQSLSLKTQEP 356
DB 271 -----RDYYD-----PF-----KGDDYNEENPTE-----PSSEGTI--SDKE 301
QY 357 LARDPVKLPPTAASPDPAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEA 416
DB 302 IVHD-VKVPPTPLPTND-VDYVLETASDADNEHARFQAKEQLEIRHRNRMDRVKKWEA 359
QY 417 EROAKNLPKADKAVIQHFOEKVESLEQEAANEROQLVETHMARVEAMLNDRRLALENY 476
DB 360 ELQAKNLPKTEROTLIQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLALENY 419
QY 477 ITPALQAVPRPRHVFNMLKKYVRAEOKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHRY 536
DB 420 LAALQSDPRPRHRIQALRRYVRAENKDRLTIRHYQHVLAVDPEKAAQMSQVMTHLHV 479
QY 537 IYERNQSLSLYNVPAVAEEIQDEVDLLOKEQNSDVLANNMISEPRISYGNALMPS 596
DB 480 IEERRNOSLTLLYKVPYVAOEIOEEIDELLQOR-----ADM-----DQFTSS 522
QY 597 LTFKTTVELLPVNGEFLDLOPVHSGADSVPAANTENEVEPYDARPADRGLTTRPGS 656
DB 523 ISENPVDVRSSESE-EIIPPHLHPF-----PSLSENE-----GSGMAEQDG- 565
QY 657 GLTNITKEEI-SEVKMDAEFRHDSGYEVHHQKLVFAEDVGS-----N 698
DB 566 GLIGAEKVINSKNKMDENMVIDETLDY--KEMIFNAERYVGLEEPESVGPLREDESLS 623
QY 699 KGAIGLMVGGVVIATVIVITLVLMLKKQYTSIHGVEVEADAAPTPEERHLISKMQONGYE 758

DB 624 SNALIGLVIATAIATVIVISLWMLRKRQYGTISHGIVEVDPMLTPPEERHLNKQNHGYE 683
QY 759 NPTYKFEEOQM 769
DB 684 NPTYKYLEQOM 694

RESULT 8
APPL_HUMAN
ID APPL_HUMAN STANDARD; PRT; 650 AA.
AC P51693; O00113;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP).
GN APLP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088960; Pubmed=9428684;
RA Paliga K., Peraus G., Kieger S., Duwrrwang U., Hesse L., Multaup G.,
RA Masters C.L., Beyreuther K., Weidemann A.;
RT "Human amyloid precursor-like protein 1-cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RT Eur. J. Biochem. 250:354-363(1997).
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=98180887; Pubmed=9521588;
RA Lenkeri U., Kestila M., Lamerdin J., McCreedy P., Adamson A.,
RA Olsen A., Trygvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RL Hum. Genet. 102:192-196(1998).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. C-TERMINALLY
CC PROCESSED IN THE GOLGI COMPLEX AND IS THEN SECRETED.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTICULARLY
CC IN THE CEREBRAL CORTEX POSTSYNAPTIC DENSITY.
CC -!- PTM: N- AND O-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL; U48437; AAB96331.1; -.
DR EMBL; AD000864; AAB50173.1; -.
DR HSSP; P05067; 1MWP.
DR MIM; 104775; -.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 650 AMYLOID-LIKE PROTEIN 1.
FT DOMAIN 22 580 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 581 603 POTENTIAL.
FT DOMAIN 604 650 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 640 643 CLATHRIN-BINDING (POTENTIAL).
FT DOMAIN 241 247 POLY-GLU.
FT DOMAIN 264 268 POLY-GLU.
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).

QY	298	GPCRAMISRMFYDVTGEGKCAPFEYGGCGGNRRNNFDTEEYCMAYCGSAMQSLLKTTQEP	357
Db	282	-----VMVSR-----VT-----	288
QY	358	ARDPVKLPTTAASTPDAVDKYLETPGDENEHAFQAKAKERLEAKHRRMSQVREWEAE	417
Db	289	---PTPRPT-----DGDVDYFGEIGEIGEGFLRAKMDLEERRMRQINEWMREWAMAD	339
QY	418	ROAKNLPKADKKAVIOHFOEKVESTLEQEAANERQOLVETHMARVEAMLNDRRLALENYI	477
Db	340	SQSKNLPKADQALNEHFQSLQTLTEEQVSGERQRLVETHATRVIALINDQRAALEGFL	399
QY	478	TALQAVPRPRHVENMLKKKYVRAEQKDRQHTLKHFEHVBMVDPKKAQTRSQVMTHLRVI	537
Db	400	AALQGDPRQAEKRVLMALRRYLRAEKEQRHTLRHYQHAAYDPEKAQOMFQVQTHLOVI	459
QY	538	YERMNOSLSLLYNVPAVAEEIODEYDELLQKEQNSDDVLANMISEPRISYGNDAIMP-S	596
Db	460	EERMNOSLGLDDQNPHLAQELRPQIOELL-----LAEHLGPSEL-----DASVPGS	505
QY	597	LTEKTTVELLPVNGEFSLLDLOQPMHSGADSVPANTENEVEVPDARPAADRGLTTRPGS	656
Db	506	SSEDK-----GSLQP-----PESKDDPPVTLP---KGSTDQESS	536
QY	657	GLTNIKTEEISEVKMDAEFRHDSGYEVHH--QKLVFAEDVGSNKGAITGLMVGVVIA	713
Db	537	SSGREKLTPLEQYEQKVNASAPRGEPFHSSDIOREDELAPSGTGVSRREALSGLLIMGAGGG	596
QY	714	TVIVITLVM-LKKQYTSIHGVEYVDAVTPPEERHLSKMOQNGYENPTYKFFEQ	767
Db	597	SLIVSLILLRKKKPYGTISHGVAYEVDPMLTLEEQQRLRELQHRHGYENPTYRLEE	651

RESULT 10	A4_DROME		STANDARD;	PRT;	886 AA.
ID	A4_DROME				
AC	P14599;				
DT	01-APR-1990 (Rel. 14, Created)				
DT	01-APR-1990 (Rel. 14, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Beta-amyloid-like protein precursor.				
GN	APPL OR VND.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
N	[1]				
NP	SEQUENCE FROM N.A.				
RX	MEDLINE=89184650; Pubmed=2494667;				
RA	Rosen D.R., Martin-Morris L., Luo L., White K.;				
RT	"A Drosophila gene encoding a protein resembling the human				
RT	beta-amyloid protein precursor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).				
RN	[2]				
RP	SEQUENCE OF 1-83 FROM N.A.				
RX	MEDLINE=91184006; Pubmed=2127912;				
RA	Martin-Morris L.E., White K.;				
RT	"The Drosophila transcript encoded by the beta-amyloid protein				
RT	precursor-like gene is restricted to the nervous system.";				
RL	Development 110:185-195(1990).				
CC	-1- FUNCTION: PROBABLY CORRESPONDS TO THE PROTEIN ENCODED BY THE				
CC	ESSENTIAL LOCUS VND, A GENE REQUIRED FOR EMBRYONIC NERVOUS				
CC	SYSTEM DEVELOPMENT.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- TISSUE SPECIFICITY: APPL TRANSCRIPTS ARE FOUND IN THE CENTRAL AND				
CC	PERIPHERAL NERVOUS SYSTEMS. WITHIN THE NERVOUS SYSTEM TRANSCRIPTS				
CC	ARE NOT OBSERVED IN NEUROBLASTS, NEWLY GENERATED NEURONS AND AT				
CC	LEAST ONE CLASS OF PRESUMED GLIAL CELLS.				
CC	-1- DEVELOPMENTAL STAGE: APPL TRANSCRIPTS ARE FOUND IN POST-MITOTIC				
CC	NEURONS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS IN ALL				
CC	DEVELOPMENTAL STAGES.				

```

CC -I SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; J04516; AAA28874.1; -.
DR EMBL; X55774; CAA39294.1; -.
DR EMBL; X55775; CAA39294.1; JOINED.
DR PTR; A32758; A32758.
DR HSSP; P05067; 1MWP.
DR FlyBase; FBgn0000108; Appl.
DR InterPro; IPR001868; A4_App.
DR Pfam; PF02177; A4_EXTRA; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Signal; Transmembrane; Amyloid; Neurogenesis.
FT SIGNAL 1 27
FT CHAIN 28 886
FT DOMAIN 28 810
FT TRANSMEM 811 833
FT DOMAIN 834 886
FT DOMAIN 876 879
FT CARBOHYD 150 150
FT CARBOHYD 161 161
FT CARBOHYD 236 236
FT CARBOHYD 239 239
FT CARBOHYD 573 573
SQ SEQUENCE 886 AA; 98261 MW; C5C1EA4194DB5A8D CRC64;

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[illegible]

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Db 436 LEEKYQDMRLADPKAQSFKQRTARFQTSVQALEEGNAEKHQLAAMHQRYLAHINOR 495
QY 469 RRLALENYITAIQAVPRPRRHVFNMLKKYVAEQKDRQHTLKHFEH-VRMVDP---KKA 524
Db 496 KREAMTCYTOALTQEPNNAHVHEKCLQKLRLALHKDRALAHYRHLNCGGPGLEAAA 555
QY 525 QIRSQVMTLRYIERMNSLSLYNPAAVEI-----ODEV----- 562
Db 556 SERPRTLRLIDRAVNQSMTMLKRPPELSAKIAQLMNDYILALRSKDDIPGSSLGMS 615
QY 563 -----DELQKEQNSDDVLAN 579
Db 616 EAEAGILDKYRVEIERKVAEKERLRLAEQKQRAERELREKRLAKKVDMLKS 675
QY 580 MISE-----PRISYGNDAIM-----PSLLETKTVELLPVNG 611
Db 676 QVAEQSQPTQSTQSQAOQQQEKSLPGKELGPDALVTANPNLETTKS----- 726
QY 612 EFSLDDLQPMHSGADSVNPANTENEVEPYDARPAADRGLTTRPGSGLTNIKTEISEVKM 671
Db 727 EKDLSDTE---YGEATVSTKVQTVLPYVDDAVQRAVEDVAAA-----VAHQEA 773
QY 672 DAEFRHDSGYEVHOKLVF-----FAEDVGSNK--GAIGLMVGVIATVIVITLVM 723
Db 774 EPQVQHFMTHDIGHRESSFSRLRFEQAHAHAKEGRNVYFTLSFAGIALMAAVFGVAVA 833
QY 724 KKKQYTSIH-HGVEVDVAVTP-----EERHLSKMOQNGYENPTYKFE 766
Db 834 KWRTRSPPHAQGFIEVDQNTTTHHPVIREEKIVPMQINGYENPTYKFE 883
```

RESULT 11

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A4_MACFA STANDARD: PRT: 87 AA.
```

```
AC P53601;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91273117; Pubmed=1905108;
RT Podlisy M.B., Tolan D.R., Selkoe D.J.;
RL "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease."
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; M58726; AAA36828.1; -.
DR PIR; S06678; S06678.
DR HSSP; P05067; 1AAP.
```

```
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1
FT DOMAIN 4 79 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 16 17 REACTIVE BOND.
FT DISULFID 6 56 BY SIMILARITY.
FT DISULFID 15 39 BY SIMILARITY.
FT DISULFID 31 52 BY SIMILARITY.
FT NON_TER 87
SQ SEQUENCE 87 AA; 9608 MW; B67C690DEE0EE7FF CRC64;
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Query Match 11.3%; Score 457; DB 1; Length 87;
Best Local Similarity 95.4%; Pred. No. 5.1e-18;
Matches 83; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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QY 286 VREVCSQAETGPCRAMISRWFVDYTEGKCAFFYGGCGGNRNFDTLEYCMVCGSAM 345
Db 1 VREVCSQAETGPCRAMISRWFVDYTEGKCAFFYGGCGGNRNFDTLEYCMVCGSYM 60
QY 346 SOSLKTTOEPLARDPVKLPPTASTP 372
Db 61 SOSLKTTRREPLTRDPVKLPPTASTP 87
```

RESULT 12

```
A4_MACMU STANDARD: PRT: 76 AA.
```

```
AC P29216;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RT Koo E.H., Sisodia S.S., Price D.L.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL; X15985; CAA34116.1; -.
DR PIR; S06678; S06678.
DR HSSP; P05067; 1TAW.
```

DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 1 76 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 13 14 REACTIVE BOND.
FT DISULFID 3 53 BY SIMILARITY.
FT DISULFID 12 36 BY SIMILARITY.
FT DISULFID 28 49 BY SIMILARITY.
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 8527 MW; 492BF3069AB082A1 CRC64;

Query Match 9.9%; Score 403; DB 1; Length 76;
Best local Similarity 94.7%; Pred. No. 2.8e-15;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 289 EVCSQAEETGPGRAMISRWFVDVTEGKCAPFFYGGCGGNRNEDTEYCMVCGSAMSQS 348
DB 1 EVCSQAEETGPGRAMISRWFVDVTEGKCAPFFYGGCGGNRNEDTEYCMVCGSAMSQS 60
OY 349 LKKTQEPPLADPEVKL 364
DB 61 LRKTTREPLTRDEVKL 76

RESULT 13
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -.
DR EMBL; X56126; CAA39591.1; -.
DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 7.2%; Score 292; DB 1; Length 59;
Best local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 ISEVKMDAEFRHDSGYEVHHQKLVPRADVGSNKGAIGLMVGVVIAIVITLVMLK 724
DB 1 ISEVKMDAEFRHDSGYEVHHQKLVPRADVGSNKGAIGLMVGVVIAIVITLVMLK 59

RESULT 14
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56129; CAA39594.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 7.1%; Score 288; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 667 SEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIAIVITLVMLK 724
|||||
DB 1 SEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIAIVITLVMLK 58

RESULT 15

A4_SHEEP STANDARD; PRT; 58 AA.
ID A4_SHEEP
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
protein (Beta-APP) (A-beta)] (Fragment).
GN APP.

OS Ovis aries (Sheep).
NC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
NC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC -----

DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; IAML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT CHAIN 1 1
FT NON_TER 1
FT FT 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58
SQ SEQUENCE 58 AA; 6300 MW; FA34209D88EBA82D CRC64;

Query Match 7.1%; Score 288; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 667 SEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIAIVITLVMLK 724
|||||
DB 1 SEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIAIVITLVMLK 58

Search completed: October 31, 2002, 10:12:24
Job time : 21.048 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 48.3026 Seconds
(without alignments)
2757.743 Million cell updates/sec

Title: US-09-785-215-2

Perfect score: 4058

Sequence: 1 MLPGLALLLLAAWTARALEV.....KMQQNGYENPTYKFFEQMQN 770

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTRMBL_19:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3981	98.1	770	6	O9TUI0 sus scrofa
2	3719.5	91.7	751	13	O9DGJ7 gallus gall
3	3590.5	88.5	695	6	O95KN7 macaca fasc
4	3522.5	86.8	695	11	O60496 cavia sp. p
5	3489.5	86.0	695	11	P97487 mus musculu
6	3403.5	83.9	747	13	O91963 xenopus. ap
7	3377.5	83.2	695	13	O9DGJ8 gallus gall
8	3163.5	78.0	693	13	O98SG0 xenopus lae
9	3152.5	77.7	695	13	O98SF9 xenopus lae
10	3065	75.5	607	11	O99K32 mus musculu
11	2914	71.8	699	13	O57394 narke japon
12	2831	69.8	547	4	O13764 homo sapien
13	2785.5	68.6	738	13	O90W28 brachydanio
14	2763.5	68.1	780	13	O73683 tetraodon f
15	2717	67.0	569	13	O9PVL1 gallus gall
16	2699	66.5	737	13	O93279 fugu rubrip

17	2562.5	63.1	534	13	O93296 gallus gall
18	2446.5	60.3	484	4	O13793 homo sapien
19	2288.5	56.4	612	13	O919E7 brachydanio
20	1960.5	48.3	763	11	O61482 mus musculu
21	1956.5	48.2	751	11	O60709 mus musculu
22	1733.5	42.7	695	4	O13861 homo sapien
23	1721	42.4	669	4	O14662 homo sapien
24	1709.5	42.1	695	11	O64348 mus musculu
25	1569	38.7	305	4	O9BT38 homo sapien
26	1302	32.1	523	4	O14594 homo sapien
27	1267	31.2	522	4	O9BT36 homo sapien
28	1159.5	28.6	650	4	O96A92 homo sapien
29	788	19.4	160	11	O9QZ78 cavia sp. p
30	786	19.4	684	5	O952X1 caenorhabdi
31	784	19.3	680	5	O10651 caenorhabdi
32	739	18.2	887	5	O9U4H3 drosophila
33	738	18.2	887	5	O9TVV0 drosophila
34	678	16.7	136	6	P79307 sus scrofa
35	661	16.3	816	5	O9W5F1 drosophila
36	561	13.8	182	11	O9CYS4 mus musculu
37	493	12.1	97	4	O13778 homo sapien
38	478	11.8	97	6	O28673 oryctolagus
39	411	10.1	82	4	P78438 homo sapien
40	402	9.9	75	4	O9UQ58 homo sapien
41	393.5	9.7	82	4	O16019 homo sapien
42	389.5	9.6	82	4	O16014 homo sapien
43	387.5	9.5	82	4	O16020 homo sapien
44	376	9.3	79	11	O35463 cricetus
45	374	9.2	74	11	O60495 cavia sp. a

ALIGNMENTS

RESULT 1	O9TUI0	PRELIMINARY:	PRT:	770 AA.
ID	O9TUI0			
AC	O9TUI0;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	AMYLOID PRECURSOR PROTEIN.			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kimura A., Takahashi T.;			
RT	"Amyloid Precursor Protein 770.";			
RL	Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AB032550; BAA84580.1; -			
DR	HSSP; P05067; IAAP.			
DR	InterPro; IPR001868; A4_APP.			
DR	InterPro; IPR002223; Kunitz_BPPI.			
DR	Pfam; PF02177; A4_EXTRA; 1.			
DR	Pfam; PF00014; Kunitz_BPPI; 1.			
DR	PRINTS; PR00203; AMYLOIDA4.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	SMART; SM0006; A4_EXTRA; 1.			
DR	SMART; SM00131; KU; 1.			
DR	PROSITE; PS00319; A4_EXTRA; 1.			
DR	PROSITE; PS00320; A4_INTRA; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 1.			
KW	Serine protease inhibitor.			
SQ	SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;			
QY	Query Match	98.1%;	Score 3981;	DB 6; Length 770;
	Best Local Similarity	97.8%;	Pred. No. 2.8e-240;	
	Matches 753; Conservative	8;	Mismatches 9;	Indels 0; Gaps 0;
	1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRILNMHNVQNGKWDSPSGTK 60			

Db	1	MLPGLALVLLAAWTARALEVPTDGNAGLAEPOVAMFCGKLNHMNVQNGKWESDPSGK	60
QY	61	TCIDTKEGILQYCEVYPELOITNVVEANQVPTIQNMCKRGKCKTHPHFVPIRCLVG	120
Db	61	TCIGTKEGILQYCEVYPELOITNVVEANQVPTIQNMCKRSRKCKCTHTHIVIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEEVEE	240
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEVAEEVEE	240
QY	241	EADDEDEDGDEVEEAEPEYEATERTSIATTTTTSVEEVEVREVCSQAETGPC	300
Db	241	EADDEDEDGDEVEEAEPEYEATERTSIATTTTTSVEEVEVREVCSQAETGPC	300
QY	301	RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMQSLSLKTQEPRLARD	360
Db	301	RAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMQSLSLKTQEPRLARD	360
QY	361	PVKLPPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA	420
Db	361	PVKLPPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAEERQA	420
QY	421	KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
Db	421	KNLPRADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL	480
QY	481	QAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYER	540
Db	481	QAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYER	540
QY	541	MNOSLSLLYNPVAVAEIQDEVELLOKEQNSDDVLANMISEPRISYNDALMPSLTET	600
Db	541	MNOSLSLLYNPVAVAEIQDEVELLOKEQNSDDVLANMISEPRISYNDALMPSLTET	600
QY	601	KTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
Db	601	KTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDPARPAADRGLTTRPGSGLTN	660
QY	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIATVIYITL	720
Db	661	IKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIATVIYITL	720
QY	721	VMLKKKOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMON	770
Db	721	VMLKKKOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMON	770

RESULT 2

ID	Q9DGJ7	PRELIMINARY:	PRT:	751 AA.
AC	Q9DGJ7			
DT	01-MAR-2001	(Tremblrel. 16, Created)		
DT	01-MAR-2001	(Tremblrel. 16, Last sequence update)		
DT	01-DEC-2001	(Tremblrel. 19, Last annotation update)		
DE	BETA-AMYLOID PRECURSOR PROTEIN	751 ISOFORM.		
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosaustra; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sarasa M., Rodolosse A., Sorribas V.;			
RT	"Cloning of full-length chicken beta-amyloid precursor protein			
RT	isoforms."			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF289219; AAC00594.1; .			
DR	HSSP: P05067; 1BA4.			

DR	InterPro: IPR001868; A4_APP.
DR	InterPro: IPR002223; Kunitz_BPTI.
DR	Pfam: PF02177; A4_EXTRA; 1.
DR	Pfam: PF00014; Kunitz_BPTI; 1.
DR	PRINTS: PR00203; AMYLOIDA4.
DR	PRINTS: PR00759; BASICPTASE.
DR	SMART: SM00006; A4_EXTRA; 1.
DR	SMART: SM00131; KU; 1.
DR	PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW	Serine protease inhibitor.
SQ	SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 91.7%; Score 3719.5; DB 13; Length 751;
Best Local Similarity 91.7%; Pred. No. 5.6e-224;
Matches 708; Conservative 18; Mismatches 23; Indels 23; Gaps 4;

QY	1	MLPGLALLLAAGTARALEVPTDGNAGLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK	60
Db	1	MLPGLALLLAAGTARALEVPTDGNAGLAEPOIAMFCGRLNMHMNVQNGKWEPSGK	60
QY	61	TCIDTKEGILQYCEVYPELOITNVVEANQVPTIQNMCKRGKCKTHPHFVPIRCLVG	120
Db	61	TCIDTKEGILQYCEVYPELOITNVVEANQVPTIQNMCKRGKCKTHPHFVPIRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQRMDVCETHLHWTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVE--VAEEVEAEVE	238
Db	181	GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVE--VAEEVEAEVE	238
QY	239	EEBADDEDGDEVEEAEPEYEATERTSIATTTTTSVEEVEVREVCSQAETG	298
Db	241	DEBADD--DDDDGDEI--EEYEYEATERTSIATTTTTSVEEVEVREVCSQAETG	298
QY	299	PCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSAMQSLSLKTQEPRLA	358
Db	299	PCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDEEYCMVCGSV-----	344
QY	359	RDDVCLPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAER	418
Db	345	-----LPTTAASTPDADVDKYLETPGDENEHAHFQAKAKERLEAKHREMSQVMREWEAER	399
QY	419	QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT	478
Db	400	QAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT	459
QY	479	ALQAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVY	538
Db	460	ALQAVPRPRRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVY	519
QY	539	ERNOSLSLLYNPVAVAEIQDEVELLOKEQNSDDVLANMISEPRISYNDALMPSLT	598
Db	520	ERNOSLSLLYNPVAVAEIQDEVELLOKEQNSDDVLANMISEPRISYNDALMPSLT	579
QY	599	EKTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDPARPAADRGLTTRPGSGL	658
Db	580	EKTTVELLPVNGEESLDDLPWHSFGADSVRPANTENEVEPVDPARPAADRGLTTRPGSGL	639
QY	659	TNKTTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIATVIYI	718
Db	640	TNKTTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVIATVIYI	699
QY	719	TLVMLKKKOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMON	770
Db	700	TLVMLKKKOYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEQMON	751

RESULT 3	
Q95KN7	PRELIMINARY: PRT: 695 AA.
ID	Q95KN7

AC Q95KN7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisy M.B., Tolian D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 88.5%; Score 3590.5; DB 6; Length 695;
Best local Similarity 90.1%; Pred. No. 5.6e-216;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPELQITNVEANQPTIQMWCKRGKQCKTHPHVPIPYRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELQITNVEANQPTIQMWCKRGKQCKTHPHVPIPYRCLVG 120
QY 121 EFVSDALVDPCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALVDPCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDDEDEGEVEEAEPEYEATEERTSTATTTTSTESVEEVREVCSEQAETGPC 300
DB 241 EADDEDDEDEGEVEEAEPEYEATEERTSTATTTTSTESVEEVREVCSEQAETGPC 300
QY 301 RAMISRWFYDVEGKCAPEFFYGGCGGNRNNEPTREYCMVCGSAMSQSLKTQEPPLARD 360
DB 289 ----- 288
QY 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
DB 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
DB 346 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVMYDPAKKAQIRSQVMTLRLVIYER 540
DB 406 QAVPRPRHVFENMLKKYVRAEQKDRQHTLKHFEHVMYDPAKKAQIRSQVMTLRLVIYER 540
QY 541 MNQSLSLYNPAPAEEIQDEVDELLQKEQNSDDVLANMISEPRISYGNALMPSLTET 600
DB 466 MNQSLSLYNPAPAEEIQDEVDELLQKEQNSDDVLANMISEPRISYGNALMPSLTET 600
QY 601 KTTVELLPVNGEFSLDLQPMHSGFADSVPAANTENEVEPVDPADPADRGTLTRPGSGLTN 660
DB 526 KTTVELLPVNGEFSLDLQPMHSGFADSVPAANTENEVEPVDPADPADRGTLTRPGSGLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAIVITL 720

DB 586 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVVIAIVITL 645
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 770
DB 646 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 4
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496
AC Q60496;

DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 86.8%; Score 3522.5; DB 11; Length 695;
Best local Similarity 88.2%; Pred. No. 9.8e-212;
Matches 679; Conservative 7; Mismatches 9; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLAEPQIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPELQITNVEANQPTIQMWCKRGKQCKTHPHVPIPYRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELQITNVEANQPTIQMWCKRGKQCKTHPHVPIPYRCLVG 120
QY 121 EFVSDALVDPCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALVDPCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDDEDEGEVEEAEPEYEATEERTSTATTTTSTESVEEVREVCSEQAETGPC 300
DB 241 EADDEDDEDEGEVEEAEPEYEATEERTSTATTTTSTESVEEVREVCSEQAETGPC 300
QY 301 RAMISRWFYDVEGKCAPEFFYGGCGGNRNNEPTREYCMVCGSAMSQSLKTQEPPLARD 360
DB 289 ----- 288
QY 361 PVKLPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
DB 289 ---VPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
QY 421 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480
DB 346 KNLPKADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAL 480

Db 644 TLVMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFFEOMQN 695

RESULT 8

ID	Q98SG0	PRELIMINARY;	PRT;	693 AA.
AC	Q98SG0;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	BETA-AMYLLOID PRECURSOR PROTEIN A.			
GN	APP.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=83355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
DR	Van den Hurk W.H.;			
DR	Thesis (2001), Department of Biological Sciences,			
DR	University of Nijmegen, Nijmegen, Netherlands.			
DR	EMBL; AJ298150; CAC37193.1; -.			
DR	HSP; P05067; 1H23.			
DR	InterPro; IPR001868; A4_APP.			
DR	Pfam; PF02177; A4_EXTRA; 1.			
DR	PRINTS; PR00203; AMYLOIDA4.			
DR	SMART; SM00006; A4_EXTRA; 1.			
DR	PROSITE; PS00319; A4_EXTRA; 1.			
DR	PROSITE; PS00320; A4_INTRA; 1.			
KW	Signal.			
FT	SIGNAL	1	18	POTENTIAL.
Q	SEQUENCE	693 AA;	78568 MW;	CAFI0F655CIAB653 CRC64;

Query Match	78.0%;	Score 3163.5;	DB 13;	Length 693;
Best Local Similarity	79.1%;	Pred. No. 2.5e-189;		
Matches 611;	Conservative 37;	Mismatches 43;	Indels 81;	Gaps 5;

Qy	1	MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFEGCRLNMHMNVQNGKWDSDSGTK	60
Db	1	MLPHITLLVLTV - GALALEVPADGNGLLAEPQIAMFEGCKILNMHMNVQNGKWTETVSGTK	59
Qy	61	TCIDTKEGILQYCOQEVYPELOITNVVEANQPTIQNMCKRGKQCKTHPHFVIRPCLVG	120
Db	60	GCIGTKEGILQYCOQEVYPELOITNVVEANQPTIQNMCKRGKQCKSRTHIVAPYRCLVG	119
Qy	121	EFVSDALIVPDKCKFLHOERMVCEETHLHMHTVAKETCSEKSTNLHDYGMLLPCGIDKFR	180
Qy	120	EFVSDALIVPDKCKFLHOERMVICETHLHMHTVAKESCSEKSMSLHEYGMLLPCGIDKFR	179
Qy	181	GVEFYCCPLAEESDNVDSADAEEDSDVMMWGADTDYADGSEDKVVEVA - -EEEEVAEVE	238
Db	180	GVEFYCCPSAEESSESFDSDA - EDDSDAMWGADADYVDRDDKAVEAQPDDEEEVEVE	238
Qy	239	EEEDADDEDDEGDEVEEEAEPEYEATERTTSIATTTTTTSEVEEVVREVCSQEAETG	298
Db	239	EEETDDED - -DGDEAEEEPEEPEYEATERTTSIATTTTTTSEVEEVV - - - - -	286
Qy	299	PCRAMISRMYEDVTEGCKAPFFYGGCGGNRNNFDTEEYCAVCGSAMSQSLKTQEPPLA	358
Db	287	-----	286
Qy	359	RDPVKLPTTAASTPDVADKYLETPGDENEHNAHFQAKAKERLEAKHREMSQVMEWEAER	418
Db	287	-----VPATAASTPDVADKYLENPDENENEHDFLKAKEKRGKHREKMSVMEWEAER	341
Qy	419	QAKNLKADKKAVIQHFQEKVESTLEQEAANERQQLVETHNARVEAMLNDRRLALENYIT	478
Db	342	QAKNLKADKKAVIQHFQEKVESTLEQEAANERQQLVETHNARVEAMLNDRRLALENYIT	401
Qy	479	ALQAVPRPRRHVENMLKKYVRAEOKDROHTLKHFEHVRAVDPKKAQIRSOVMTHLRYIY	538
Db	402	ALQADPRPRRHVENMLKKYVRAEOKDROHTLKHFEHVRAVDPKKAQIRSOVMTHLRYIN	461

[illegible]

RESULT 9

ID	Q98SF9	PRELIMINARY;	PRT;	695 AA.
AC	Q98SF9;			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	BETA-AMYLOID PRECURSOR PROTEIN B. APP.			
GN	Xenopus laevis (African clawed frog).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			

RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
RL

DR	HSSP; P05067; 1H23.	
DR	InterPro; IPR001868; A4_APP.	
DR	Pfam; PF02177; A4_EXTRA; 1.	
DR	PRINTS; PR00203; AMYLOIDA4.	
DR	SMART; SM00006; A4_EXTRA; 1.	
DR	PROSITE; PS00319; A4_EXTRA; 1.	
DR	PROSITE; PS00320; A4_INTRA; 1.	
KW	Signal.	
FT	SIGNAL.	
SQ	SEQUENCE	695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match	77.7%;	Score 3152.5;	DB 13;	Length 695;
Best Local Similarity	78.9%;	Pred. No. 1.2e-188;		
Matches 609;	Conservative 39;	Mismatches 45;	Indels 79;	Gaps 5;

QY	1	MLPGLALLLLAAWMTARALEVYPIDGNAGLLAEPQIAMFCGRILNMHMNVONGKWDSPSGTK	60
		: : : :	
Dd	1	MLPHITLLLVTA -GALALEVPADNGGLLAEPQIAMFCGKLNMHMNVONGKWEVDVSGTK	59
QY	61	TCIDTKEGILQYCOEVYPELOITNVEANQPVTIQNMCKRGKOCKTHPFVIPIRCLVG	120
		: : :	
Dd	60	GCIGTKEGILOQCQEVYPELOITNVEANQPVTIQNMCKKGKOKCSRTHIVIPYRCLVG	119
QY	121	EFSVDALLVPDKCKFLHOERMVCEThLHWHTVAKETCSEKSTNLHDYGMLLPBGIDKFR	180
		: : :	
Dd	120	EFSVDALLVPDKCKFLHOERMVICETHLHWHTVAKESCSSEKIMSLHEXGMILLPCGIDKFR	179
QY	181	GVEFVCCPLAEESDNVDSADAEEDDSDVWMWGADTDYADGSSEDKVVEV--AEEEEVAEVE	238
		: :	
Dd	180	GVEFVCCPTAESESSEFDSADA -EDSDVWMWGADADYVDRSDKAENAQPEEEBEVEVE	238
QY	239	EEAADDEDDEDEDGEVEEAAPYEATERTTSIATTTTTTESVEEYVRVCSEQAETG	298
		:	
Dd	239	EEAADDD -DEDDGETEEEBEPYEATERITSIATTTTTTTESVEEVRV-----	289

OS Unidentified.
XX
PN WO200052048-A1.
XX 08-SEP-2000.
PD
XX 03-MAR-2000; 2000WO-US05574.
PF
XX 04-MAR-1999; 99US-0122736.
PR
XX (PRAE-) PRAECIS PHARM INC.
PA
XX
PI Findeis MA, Phillips K, Olson GL, Self C;
XX
DR WPI; 2000-594168/56.
XX
XX
PT Novel compounds that are useful as modulators of beta-amyloid peptide
XX aggregation in treating amyloidosis, comprises D-amino acids
XX
XX Disclosure; Page 9; 87pp; English.
XX
XX The present sequence is beta-amyloid peptide. The present invention
XX relates to peptides (see AAB27023-B27046) that modulate beta-amyloid
XX peptide aggregation, and hence inhibit the neurotoxicity of beta-amyloid
XX peptide. The beta-amyloid peptide modulators would be useful for
XX treating disorders associated with beta-amyloidosis for e.g. Alzheimer's
XX disease. The present sequence is derived from amyloid precursor protein
XX via proteolysis. The gene for amyloid precursor protein maps to
XX chromosome 21.
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 14
AAB15372
ID AAB15372 standard; peptide; 43 AA.
XX
XX AAB15372;
XX
XX 17-JAN-2001 (first entry)
XX
XX Human beta-amyloid precursor protein A-beta fragment.
XX
XX Human; beta-amyloid precursor protein; beta-APP; Alzheimer's disease;
XX chromosome 21; epitope.
XX
XX Homo sapiens.
XX
XX WO200042166-A2.
XX
XX 20-JUL-2000.
XX
XX 13-JAN-2000; 2000WO-US00872.
XX
XX 13-JAN-1999; 99US-0115749.
XX
XX (DUPO) DUPONT PHARM CO.
XX
XX Selffert DA, Mitchell TJ;
XX
XX WPI; 2000-476049/41.
XX
XX A cDNA construct that encodes beta-amyloid precursor protein for
XX identifying compounds which inhibit A-beta peptide release and/or
XX synthesis comprises an epitope tag within the A-beta sequence -
PT

XX
PS Disclosure; Page 13-14; 42pp; English.
XX
XX The present sequence is A-beta fragment of the human beta-amyloid
XX precursor protein (beta-APP). It was used in the production of peptides
XX of the invention. The invention concerns the production, detection and
XX characterisation of epitope-tagged beta-APP proteins, and their use in
XX identifying modulators of beta-APP which can be used to treat diseases
XX associated with an altered metabolism of the protein, in particular
XX Alzheimer's disease.
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 15
AAB21216
ID AAB21216 standard; peptide; 43 AA.
XX
XX AAB21216;
XX
XX 11-JAN-2001 (first entry)
XX
XX Beta-amyloid peptide.
XX
XX Beta-amyloid peptide; membrane-spanning glycoprotein; analgesic;
XX nicotinic agonist; beta-amyloid precursor protein; APP;
XX Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX US6117901-A.
XX
XX 12-SEP-2000.
XX
XX 21-NOV-1997; 97US-0976179.
XX
XX 22-NOV-1996; 96US-0098551.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
XX (ELIL) LILLY & CO ELI.
XX
XX Thorsett ED, Nissen JS, Wu J, Latimer LH, John V, Fang LY;
XX Audia JE, Mabry TE;
XX
XX WPI; 2000-637551/61.
XX
XX Eliciting analgesic effect in mammal, e.g. human, involves
XX administering an aryl substituted olefinic amine compound -
XX
XX Disclosure; Column 11; 32pp; English.
XX
XX The present sequence is the beta-amyloid peptide, which is part of
XX a large membrane-spanning glycoprotein, referred to as the beta-amyloid
XX precursor protein (APP). Aryl substituted olefinic amine (metanicoline)
XX compounds which inhibit beta-amyloid peptide release and/or its
XX synthesis may be useful for treating Alzheimer's disease, both
XX prophylactically and therapeutically.
XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

|||||
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAILGLMVGCVIAT 43

Search completed: October 31, 2002, 10:12:01
Job time : 5.01476 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 2.69742 Seconds
(without alignments)
2757.743 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	222	100.0	82	4	P78438	P78438 homo sapien
2	222	100.0	82	4	Q16014	Q16014 homo sapien
3	222	100.0	82	4	Q16019	Q16019 homo sapien
4	222	100.0	82	4	Q16020	Q16020 homo sapien
5	222	100.0	534	13	O93296	O93296 gallus gall
6	222	100.0	695	6	Q95KN7	Q95KN7 macaca fasc
7	222	100.0	695	11	Q60496	Q60496 cavia sp. p
8	222	100.0	695	13	Q9DGJ8	Q9DGJ8 gallus gall
9	222	100.0	751	13	Q9DGJ7	Q9DGJ7 gallus gall
10	222	100.0	770	6	Q9TUI0	Q9TUI0 sus scrofa
11	217	97.7	569	13	Q9PVL1	Q9PVL1 gallus gall
12	212	95.5	97	4	Q13778	Q13778 homo sapien
13	203	91.4	79	11	O35463	O35463 cricetus
14	203	91.4	607	11	O99K32	O99K32 mus musculu
15	203	91.4	693	13	Q98SG0	Q98SG0 xenopus lae
16	203	91.4	695	11	P97487	P97487 mus musculu

17	203	91.4	747	13	Q91963	Q91963 xenopus . ap
18	200	90.1	695	13	Q98SF9	Q98SF9 xenopus lae
19	193	86.9	699	13	O57394	O57394 narke japon
20	180	81.1	780	13	O73683	O73683 tetraodon f
21	176	79.3	33	4	Q9UC33	Q9UC33 homo sapien
22	176	79.3	737	13	O93279	O93279 fuigu rubrip
23	162.5	73.2	612	13	Q919E7	Q919E7 brachydanio
24	162.5	73.2	738	13	Q90W28	Q90W28 brachydanio
25	162	73.0	30	4	Q9UCA9	Q9UCA9 homo sapien
26	147	66.2	28	4	Q9UCD1	Q9UCD1 homo sapien
27	126	56.8	49	6	O97917	O97917 bos taurus
28	106	47.7	19	4	Q9UCB6	Q9UCB6 homo sapien
29	64	28.8	20	4	Q9UCB6	Q9UCB6 homo sapien
30	64	28.8	328	2	Q9RPS4	Q9RPS4 enterococcu
31	64	28.8	755	2	Q9R694	Q9R694 agrobacteri
32	64	28.8	755	2	Q9R717	Q9R717 agrobacteri
33	64	28.8	755	2	Q9R472	Q9R472 agrobacteri
34	62	27.9	755	2	Q44388	Q44388 agrobacteri
35	61	27.5	755	2	Q9WWA1	Q9WWA1 agrobacteri
36	57.5	25.9	895	10	Q9AWB6	Q9AWB6 lycopersico
37	57	25.7	195	10	O22662	O22662 arabidopsis
38	57	25.7	332	12	Q9DQNS	Q9DQNS potato viru
39	57	25.7	365	12	Q9WG05	Q9WG05 potato viru
40	57	25.7	575	10	O81120	O81120 lotus japon
41	55.5	25.0	678	16	O84344	O84344 chlamydia t
42	55	24.8	291	16	Q97T23	Q97T23 streptococc
43	55	24.8	738	16	Q92VFI	Q92VFI rhizobium m
44	54.5	24.5	678	16	Q9PK54	Q9PK54 chlamydia m
45	54.5	24.5	829	10	Q9XGTO	Q9XGTO gossypium h

ALIGNMENTS

RESULT 1						
P78438						
ID	P78438	PRELIMINARY;	PRT;	82	AA.	
AC	P78438;					
DT	01-MAY-1997 (TREMBLrel. 03, Created)					
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)					
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)					
DE	AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).					
GN	APP.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=89392030; PubMed=2675837;					
RA	Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,					
RA	Little S.P.;					
RT	"Alzheimer's disease amyloid peptide is encoded by two exons and shows					
RT	similarity to soybean trypsin inhibitor.";					
RL	Biochem. Biophys. Res. Commun. 163:1248-1255(1989).					
RN	[2]					
RP	SEQUENCE OF 19-48 FROM N.A.					
RX	MEDLINE=87120329; PubMed=2949367;					
RA	Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,					
RA	Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;					
RT	"Amyloid beta protein gene: cDNA, mRNA distribution, and genetic					
RT	linkage near the Alzheimer locus.";					
RL	Science 235:880-884(1987).					
RN	[3]					
RP	SEQUENCE OF 32-63 FROM N.A.					
RX	MEDLINE=93035397; PubMed=1415269;					
RA	Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,					
RA	Anderson L., O'dahl S., Nemens E., White J.A.;					
RT	"Linkage and mutational analysis of familial Alzheimer disease					
RT	kindreds for the APP gene region.";					
RL	Am. J. Hum. Genet. 51:998-1014(1992).					
DR	EMBL; M29270; AAA51768.1; -.					
DR	EMBL; M29269; AAA51768.1; JOINED.					

DR EMBL; M15532; AAA51564.1; -
DR EMBL; S45136; AAB23646.1; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 17 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 59

RESULT 2

ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 3

ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82

SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 4

ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
Db 18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 60

RESULT 5

ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 436 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 478

RESULT 6

Q95KN7

ID Q95KN7 PRELIMINARY; PRT; 695 AA.

AC Q95KN7; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;

RP [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).

DR EMBL; M58727; AAA36829.1; -
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 7

Q60496

ID Q60496 PRELIMINARY; PRT; 695 AA.

AC Q60496; 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.

OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE=97236426; PubMed=9116031;

RA Beck M., Mueller D., Bigl V.;

RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";

RL Biochim. Biophys. Acta 1351:17-21(1997).

DR EMBL; X97631; CAA66230.1; -

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 222; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 8

Q9DGJ8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.

AC Q9DGJ8; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Sarasa M., Rodolose A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF289218; AAG00593.1; -

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR Pfam; PF02177; A4_EXTRA; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 9

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.

AC Q9DGJ7; 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Sarasa M., Rodolose A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF289219; AAG00594.1; -

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 653 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 695

SUULT 10

O9TUI0 PRELIMINARY; PRT; 770 AA.

ID O9TUI0
AC O9TUI0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; LAAP.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 222; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 672 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 714

RESULT 11

O9PVL1 PRELIMINARY; PRT; 569 AA.

ID O9PVL1
AC O9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 97.7%; Score 217; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 42
DB 472 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIA 513

RESULT 12

O13778 PRELIMINARY; PRT; 97 AA.

ID O13778
AC O13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Galjusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 95.5%; Score 212; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 EFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 41

RESULT 13

O35463 PRELIMINARY; PRT; 79 AA.

ID O35463
AC O35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
GN	BETA APP.
OS	Cricetulus griseus (Chinese hamster).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC	Cricetulus.
OX	NCBI_TaxID=10029;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Sambamurti K., Pinnix I., Gandhi S.;
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF030413; AAB86608.1; -.
DR	HSSP; P05067; 1BA4.
FT	NON_TER 1 1
FT	NON_TER 79 79
SQ	SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

	Query Match	91.4%;	Score 203;	DB 11;	Length 79;
	Best Local Similarity	93.0%;	Pred. No. 3.4e-19;		
	Matches 40;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1 DAEFRHDSGEVHHOKLVFFAEDVGSNKGAIIGLMVGGVVIAT				43
Dd	21 DAEFGHDSGFEVRHQKLVEFAEDVGSNKGAIIGLMVGGVVIAT				63

RESULT 14
Q99K32

ID Q09K32 PRELIMINARY; PRT; 607 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -.

DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match	91.48;	Score 203;	DB 11;	Length 607;
Best Local Similarity	93.08;	Pred. No. 3.6e-18;		
Matches 40; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

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Oy 1 DAEFRHDSGYEYHHOKLVFEAFEDVGSNKGAITGLMWGVVIAT 43
    ||| |||:| | ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 DAEFGHDSGEFEYHHOKLVFEAFEDVGSNKGAITGLMWGVVIAT 551

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RESULT 15	
Q98SG0	
ID Q98SG0	PRELIMINARY; PRT; 693 AA

AC	Q98SG0;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	BETA-AMYLOID PRECURSOR PROTEIN A.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; --
DR HSSP: P05067; 1HZ3.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Signal.
FT SIGNAL. 1 18 POTENTIAL.
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655CIAB653 CRC64;

Query Match	91.4%;	Score 203;	DB 13;	Length 693;
Best Local Similarity	88.4%;	Pred. No. 4.1e-18;		
Matches 38; Conservative	4;	Mismatches 1;	Indels 0;	Gaps 0;

DQ **I** DAEFRHDSGYEVHHÖKQLVFEADVGSNKGAIIGLMWGVVIAT 43
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 595 DSEYRHDYALVEVHHÖKLVFFAEEVGSNKGAIIGLMWGVVIAT 637

Search completed: October 31, 2002, 10:14:35
Job time : 4.69742 secs

